SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
1072	31440	B	1086	132	1200	
1073	31441	B	1087	95	418	
1074	31442	B	1088	26	56	
1075	31443	B	1089	1	873	
1076	31444	C	1090	107	196	
1077	31445	B	1091	157	777	
1078	31446	B	1092	1	1273	
1079	31447	B	1093	1	202	
1080	31448	B	1094	1	382	
1081	31449	C	1095	189	449	
1082	31450	C	1096	325	429	
1083	31451	C	1097	3	80	
1084	31452	B	1098	50	691	
1085	31453	B	1099	1	474	
1086	31454	B	1100	3	335	
1087	31455	B	1101	137	617	
1088	31456	C	1102	69	134	
1089	31457	B	1103	369	886	
1090	31458	B	1104	1	1332	
1091	31459	B	1105	106	584	
1092	31460	C	1106	97	420	
1093	31461	C	1107	142	381	
1094	31462	B	1108	214	2544	
1095	31463	B	1109	238	1323	
1096	31464	B	1110	1	3000	
1097	31465	B	1111	203	313	
1098	31466	B	1112	288	375	
1099	31467	B	1113	1	480	
1100	31468	C	1114	286	351	
1101	31469	B	1115	59	376	
1102	31470	C	1116	287	504	
1103	31471	B	1117	878	2032	
1104	31472	B	1118	52	648	
1105	31473	B	1119	1	207	
1106	31474	C	1120	1	492	
1107	31475	B	1121	46	830	
1108	31476	B	1122	1	525	
1109	31477	B	1123	1	930	
1110	31478	C	1124	157	606	
1111	31479	C	1125	70	405	
1112	31480	C	1126	247	411	
1113	31481	C	1127	339	590	
1114	31482	B	1128	1	1881	
1115	31483	C	1129	258	452	
1116	31484	B	1130	241	733	
1117	31485	C	1131	294	530	
1118	31486	B	1132	1	439	
1119	31487	B	1133	16	612	
1120	31488	C	1134	234	377	
1121	31489	B	1135	134	763	
1122	31490	C	1136	1	228	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
1123	31491	B	1137	63	443	
1124	31492	C	1138	30	269	
1125	31493	B	1139	44	151	
1126	31494	B	1140	69	199	
1127	31495	B	1141	347	2830	
1128	31496	B	1142	1	576	
1129	31497	C	1143	49	129	
1130	31498	B	1144	1	1107	
1131	31499	B	1145	17	153	
1132	31500	B	1146	277	694	
1133	31501	B	1147	1	735	
1134	31502	B	1148	1	1110	
1135	31503	B	1149	55	552	
1136	31504	C	1150	463	591	
1137	31505	B	1151	136	266	
1138	31506	B	1152	1	795	
1139	31507	B	1153	128	880	
1140	31508	C	1154	178	366	
1141	31509	B	1155	1	654	
1142	31510	B	1156	1	3294	
1143	31511	B	1157	16	854	
1144	31512	B	1158	1093	1185	
1145	31513	B	1159	1	930	
1146	31514	B	1160	1	3969	
1147	31515	B	1161	1	4173	
1148	31516	B	1162	1	2187	
1149	31517	B	1163	47	993	
1150	31518	B	1164	1	1241	
1151	31519	B	1165	46	2170	
1152	31520	B	1166	1	1781	
1153	31521	B	1167	179	583	
1154	31522	C	1168	167	442	
1155	31523	B	1169	44	1848	
1156	31524	C	1170	1	417	
1157	31525	B	1171	1	198	
1158	31526	B	1172	231	452	
1159	31527	B	1173	219	326	
1160	31528	B	1174	212	302	
1161	31529	B	1175	748	1084	
1162	31530	B	1176	1	540	
1163	31531	C	1177	21	143	
1164	31532	B	1178	76	1300	
1165	31533	B	1179	1	1324	
1166	31534	B	1180	1	1065	
1167	31535	B	1181	1	1263	
1168	31536	B	1182	1	1809	
1169	31537	B	1183	10	406	
1170	31538	B	1184	65	287	
1171	31539	B	1185	25	337	
1172	31540	B	1186	59	698	
1173	31541	C	1187	329	527	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
1174	31542	B	1188	1	1068	
1175	31543	B	1189	72	330	
1176	31544	B	1190	14	239	
1177	31545	B	1191	1	919	
1178	31546	B	1192	462	786	
1179	31547	B	1193	1	3468	
1180	31548	B	1194	16	457	
1181	31549	B	1195	1	697	
1182	31550	C	1196	1	145	
1183	31551	B	1197	91	450	
1184	31552	B	1198	1	1050	
1185	31553	B	1199	101	428	
1186	31554	B	1200	41	205	
1187	31555	B	1201	358	1082	
1188	31556	B	1202	1	183	
1189	31557	B	1203	1	1053	
1190	31558	B	1204	73	336	
1191	31559	B	1205	553	1587	
1192	31560	C	1206	118	366	
1193	31561	B	1207	1	423	
1194	31562	B	1208	120	338	
1195	31563	B	1209	1	1665	
1196	31564	B	1210	1	639	
1197	31565	B	1211	1	660	
1198	31566	B	1212	11	434	
1199	31567	B	1213	1	567	
1200	31568	B	1214	1	801	
1201	31569	C	1215	56	177	
1202	31570	B	1216	439	678	
1203	31571	B	1217	20	201	
1204	31572	B	1218	74	267	
1205	31573	B	1219	74	325	
1206	31574	B	1220	37	340	
1207	31575	B	1221	1	588	
1208	31576	B	1222	136	294	
1209	31577	B	1223	238	392	
1210	31578	B	1224	109	1394	
1211	31579	C	1225	300	653	
1212	31580	B	1226	32	3327	
1213	31581	B	1227	497	1306	
1214	31582	C	1228	1	333	
1215	31583	C	1229	1	249	
1216	31584	C	1230	1	249	
1217	31585	B	1231	147	297	
1218	31586	B	1232	1	714	
1219	31587	B	1233	1	1587	
1220	31588	C	1234	103	243	
1221	31589	C	1235	133	509	
1222	31590	B	1236	1	1594	
1223	31591	B	1237	1	628	
1224	31592	B	1238	1	948	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
1225	31593	B	1239	382	1020	
1226	31594	B	1240	163	5459	
1227	31595	B	1241	1	1386	
1228	31596	B	1242	44	344	
1229	31597	B	1243	6	398	
1230	31598	B	1244	77	468	
1231	31599	B	1245	520	2001	
1232	31600	B	1246	1	645	
1233	31601	B	1247	91	690	
1234	31602	B	1248	70	382	
1235	31603	B	1249	183	427	
1236	31604	B	1250	159	621	
1237	31605	B	1251	34	259	
1238	31606	B	1252	155	496	
1239	31607	B	1253	1	1416	
1240	31608	C	1254	18	355	
1241	31609	C	1255	665	826	
1242	31610	B	1256	1	559	
1243	31611	B	1257	343	1329	
1244	31612	B	1258	1	265	
1245	31613	B	1259	1	5081	
1246	31614	B	1260	373	1395	
1247	31615	B	1261	83	373	
1248	31616	B	1262	298	1252	
1249	31617	C	1263	142	327	
1250	31618	B	1264	1	237	
1251	31619	C	1265	1	330	
1252	31620	C	1266	20	358	
1253	31621	C	1267	347	493	
1254	31622	B	1268	220	1314	
1255	31623	B	1269	1	1244	
1256	31624	B	1270	35	368	
1257	31625	B	1271	145	444	
1258	31626	B	1272	1	657	
1259	31627	B	1273	84	273	
1260	31628	C	1274	47	148	
1261	31629	B	1275	1	528	
1262	31630	B	1276	34	1370	
1263	31631	C	1277	81	299	
1264	31632	C	1278	22	201	
1265	31633	B	1279	1	672	
1266	31634	B	1280	1	753	
1267	31635	C	1281	14	79	
1268	31636	C	1282	61	227	
1269	31637	B	1283	95	1124	
1270	31638	B	1284	1	891	
1271	31639	B	1285	1	1323	
1272	31640	B	1286	11	127	
1273	31641	B	1287	281	437	
1274	31642	C	1288	62	136	
1275	31643	B	1289	251	874	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
1276	31644	C	1290	16	231	
1277	31645	C	1291	299	412	
1278	31646	B	1292	310	968	
1279	31647	B	1293	237	1802	
1280	31648	B	1294	337	1143	
1281	31649	C	1295	75	176	
1282	31650	C	1296	193	414	
1283	31651	C	1297	98	679	
1284	31652	B	1298	186	260	
1285	31653	B	1299	1	732	
1286	31654	B	1300	123	268	
1287	31655	C	1301	1	420	
1288	31656	C	1302	86	223	
1289	31657	B	1303	1	594	
1290	31658	B	1304	1	4464	
1291	31659	C	1305	1	531	
1292	31660	B	1307	1	780	
1293	31661	C	1308	1	249	
1294	31662	B	1309	1	139	
1295	31663	B	1310	1	156	
1296	31664	B	1311	38	403	
1297	31665	B	1312	128	1089	
1298	31666	C	1313	262	429	
1299	31667	C	1314	209	592	
1300	31668	B	1315	1	684	
1301	31669	C	1316	1	339	
1302	31670	C	1317	71	310	
1303	31671	B	1318	1	476	
1304	31672	B	1319	133	198	
1305	31673	B	1320	1	227	
1306	31674	C	1321	612	977	
1307	31675	C	1322	65	523	
1308	31676	C	1323	35	121	
1309	31677	B	1324	8	430	
1310	31678	C	1325	1	438	
1311	31679	B	1326	1935	3296	
1312	31680	B	1332	254	462	
1313	31681	B	1333	1006	1540	
1314	31682	B	1335	127	1799	
1315	31683	B	1336	221	402	
1316	31684	C	1337	1	567	
1317	31685	C	1338	193	342	
1318	31686	B	1339	652	775	
1319	31687	B	1340	1	552	
1320	31688	B	1341	83	318	
1321	31689	B	1342	166	352	
1322	31690	C	1343	1	228	
1323	31691	B	1344	25	244	
1324	31692	C	1345	58	285	
1325	31693	B	1346	34	822	
1326	31694	B	1347	1	1563	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
1327	31695	B	1348	229	1185	
1328	31696	B	1349	59	819	
1329	31697	B	1350	1	5955	
1330	31698	B	1351	1	654	
1331	31699	B	1352	1	1299	
1332	31700	B	1353	943	1872	
1333	31701	B	1354	1	942	
1334	31702	B	1355	444	560	
1335	31703	B	1356	1	1605	
1336	31704	B	1357	1	831	
1337	31705	C	1358	48	383	
1338	31706	C	1359	1	318	
1339	31707	B	1360	186	470	
1340	31708	C	1361	1	321	
1341	31709	B	1362	1	720	
1342	31710	B	1363	1	939	
1343	31711	B	1364	1	576	
1344	31712	B	1365	1	114	
1345	31713	B	1366	129	588	
1346	31714	B	1367	24	724	
1347	31715	B	1368	1	1840	
1348	31716	B	1369	14	350	
1349	31717	B	1370	1	3187	
1350	31718	C	1371	1	261	
1351	31719	B	1372	117	890	
1352	31720	B	1373	1	438	
1353	31721	B	1374	1	217	
1354	31722	B	1375	1	160	
1355	31723	C	1376	6	191	
1356	31724	B	1377	1	759	
1357	31725	B	1378	10	251	
1358	31726	B	1379	1	719	
1359	31727	C	1380	425	886	
1360	31728	C	1381	1	216	
1361	31729	C	1382	38	229	
1362	31730	B	1383	38	672	
1363	31731	B	1384	1	1845	
1364	31732	B	1385	1	2590	
1365	31733	B	1386	32	108	
1366	31734	C	1387	215	460	
1367	31735	B	1388	1	1008	
1368	31736	B	1389	1	368	
1369	31737	B	1390	44	2402	
1370	31738	B	1391	80	1617	
1371	31739	C	1392	199	531	
1372	31740	B	1393	1	465	
1373	31741	C	1394	415	612	
1374	31742	B	1395	16	147	
1375	31743	B	1396	1	1314	
1376	31744	B	1397	1	465	
1377	31745	B	1398	1	1569	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
1378	31746	B	1399	1	490	
1379	31747	B	1400	405	573	
1380	31748	B	1401	1	2106	
1381	31749	B	1402	1	1593	
1382	31750	B	1403	1	666	
1383	31751	B	1404	1	652	
1384	31752	B	1405	352	1239	
1385	31753	B	1406	1	3184	
1386	31754	B	1407	467	1433	
1387	31755	B	1408	95	428	
1388	31756	C	1409	164	208	
1389	31757	C	1410	118	511	
1390	31758	C	1411	339	431	
1391	31759	B	1412	1	396	
1392	31760	B	1413	1	663	
1393	31761	B	1414	1	864	
1394	31762	C	1415	1	471	
1395	31763	B	1416	1	642	
1396	31764	B	1417	594	1764	
1397	31765	B	1418	1	771	
1398	31766	B	1419	1	5131	
1399	31767	B	1420	60	617	
1400	31768	B	1421	587	1202	
1401	31769	C	1422	336	638	
1402	31770	C	1423	30	200	
1403	31771	B	1424	1	1363	
1404	31772	B	1425	1	1113	
1405	31773	B	1426	1	1101	
1406	31774	B	1427	575	805	
1407	31775	C	1428	1	149	
1408	31776	C	1429	1	294	
1409	31777	C	1430	228	469	
1410	31778	B	1431	182	518	
1411	31779	B	1432	239	448	
1412	31780	B	1433	1	434	
1413	31781	C	1434	24	290	
1414	31782	C	1435	334	459	
1415	31783	B	1436	69	320	
1416	31784	B	1437	1	426	
1417	31785	B	1438	605	1423	
1418	31786	C	1439	9	113	
1419	31787	B	1440	1	58	
1420	31788	B	1441	1	210	
1421	31789	B	1442	1	2985	
1422	31790	C	1443	152	292	
1423	31791	B	1444	57	849	
1424	31792	C	1445	41	142	
1425	31793	C	1446	38	341	
1426	31794	C	1447	220	450	
1427	31795	C	1448	154	469	
1428	31796	B	1449	139	1023	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
1429	31797	B	1450	55	2370	
1430	31798	B	1451	1	1707	
1431	31799	B	1452	566	2356	
1432	31800	B	1453	72	255	
1433	31801	B	1454	51	182	
1434	31802	B	1455	466	600	
1435	31803	B	1456	481	1209	
1436	31804	B	1457	1	1638	
1437	31805	B	1458	8	874	
1438	31806	B	1459	1	552	
1439	31807	B	1460	1	2566	
1440	31808	B	1461	85	270	
1441	31809	B	1462	159	392	
1442	31810	B	1463	88	459	
1443	31811	B	1464	131	406	
1444	31812	B	1465	69	194	
1445	31813	B	1466	59	3134	
1446	31814	B	1467	1	3097	
1447	31815	B	1468	328	519	
1448	31816	C	1469	40	436	
1449	31817	B	1470	1	981	
1450	31818	B	1471	30	285	
1451	31819	B	1475	93	932	
1452	31820	B	1476	1	369	
1453	31821	C	1477	102	227	
1454	31822	B	1478	613	679	
1455	31823	B	1479	51	587	
1456	31824	C	1480	3	188	
1457	31825	B	1481	1	1434	
1458	31826	C	1482	27	173	
1459	31827	C	1483	294	503	
1460	31828	C	1484	506	718	
1461	31829	C	1485	97	504	
1462	31830	C	1486	27	185	
1463	31831	B	1487	50	3247	
1464	31832	B	1488	1	1032	
1465	31833	B	1489	8	95	
1466	31834	B	1490	17	303	
1467	31835	B	1491	34	81	
1468	31836	B	1492	1	1110	
1469	31837	B	1493	1	928	
1470	31838	C	1494	498	704	
1471	31839	B	1495	4	747	
1472	31840	B	1496	1	933	
1473	31841	B	1497	137	687	
1474	31842	B	1498	1524	1676	
1475	31843	B	1499	1	156	
1476	31844	B	1500	1	1126	
1477	31845	B	1501	122	765	
1478	31846	B	1503	95	304	
1479	31847	B	1504	1	156	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
1480	31848	C	1505	12	173	
1481	31849	B	1506	10	252	
1482	31850	B	1507	25	301	
1483	31851	B	1508	34	267	
1484	31852	B	1509	10	366	
1485	31853	B	1510	536	2776	
1486	31854	B	1511	1	276	
1487	31855	B	1512	1	420	
1488	31856	B	1513	235	363	
1489	31857	B	1514	664	741	
1490	31858	C	1515	312	452	
1491	31859	B	1516	1	504	
1492	31860	B	1517	52	346	
1493	31861	B	1518	458	1283	
1494	31862	B	1519	324	473	
1495	31863	B	1520	137	286	
1496	31864	B	1521	1	2682	
1497	31865	B	1522	352	1132	
1498	31866	B	1523	245	397	
1499	31867	C	1524	371	661	
1500	31868	B	1525	69	325	
1501	31869	B	1526	38	997	
1502	31870	B	1527	1	1753	
1503	31871	B	1528	215	2588	
1504	31872	C	1529	38	124	
1505	31873	C	1530	33	317	
1506	31874	C	1531	224	379	
1507	31875	B	1532	1	480	
1508	31876	C	1533	145	256	
1509	31877	C	1534	64	198	
1510	31878	B	1535	1	394	
1511	31879	C	1536	1	696	
1512	31880	B	1537	67	246	
1513	31881	C	1538	95	253	
1514	31882	B	1539	145	476	
1515	31883	C	1540	1	361	
1516	31884	C	1541	1	276	
1517	31885	B	1542	1	658	
1518	31886	B	1543	1	623	
1519	31887	C	1544	187	465	
1520	31888	C	1545	1	207	
1521	31889	C	1546	24	512	
1522	31890	C	1547	20	121	
1523	31891	B	1548	1	785	
1524	31892	B	1549	1	498	
1525	31893	C	1550	17	118	
1526	31894	C	1551	1	291	
1527	31895	B	1552	1	504	
1528	31896	B	1553	62	413	
1529	31897	B	1554	1	282	
1530	31898	C	1555	236	408	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
1531	31899	C	1556	220	398	
1532	31900	C	1557	1	732	
1533	31901	C	1558	1	372	
1534	31902	B	1559	1	1086	
1535	31903	C	1560	286	642	
1536	31904	B	1561	8	339	
1537	31905	B	1562	16	88	
1538	31906	C	1563	227	405	
1539	31907	B	1564	253	693	
1540	31908	C	1565	1	129	
1541	31909	B	1566	1	390	
1542	31910	B	1567	1	1377	
1543	31911	C	1568	16	264	
1544	31912	C	1569	51	269	
1545	31913	C	1570	39	266	
1546	31914	B	1571	200	260	
1547	31915	B	1572	220	372	
1548	31916	B	1573	1	377	
1549	31917	C	1574	280	441	
1550	31918	C	1575	50	131	
1551	31919	C	1576	47	265	
1552	31920	C	1577	10	291	
1553	31921	B	1578	1	522	
1554	31922	B	1579	756	1166	
1555	31923	B	1580	382	1228	
1556	31924	B	1581	63	229	
1557	31925	B	1582	1	452	
1558	31926	C	1583	299	556	
1559	31927	B	1584	1	870	
1560	31928	B	1585	1	708	
1561	31929	C	1586	1	420	
1562	31930	B	1587	1	1011	
1563	31931	C	1588	84	176	
1564	31932	C	1589	52	201	
1565	31933	C	1590	55	154	
1566	31934	C	1591	1	390	
1567	31935	C	1592	15	317	
1568	31936	B	1593	1	501	
1569	31937	B	1594	306	398	
1570	31938	B	1595	204	402	
1571	31939	C	1596	30	155	
1572	31940	B	1597	1	2274	
1573	31941	B	1598	1	486	
1574	31942	C	1599	148	504	
1575	31943	C	1600	82	282	
1576	31944	C	1601	82	282	
1577	31945	B	1602	66	395	
1578	31946	B	1603	114	237	
1579	31947	B	1604	1	1326	
1580	31948	B	1605	1	1900	
1581	31949	B	1606	1	1548	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
1582	31950	B	1607	1	1440	
1583	31951	B	1608	1	1878	
1584	31952	C	1609	402	563	
1585	31953	B	1610	1	2964	
1586	31954	B	1611	1	1284	
1587	31955	C	1612	144	449	
1588	31956	B	1613	1	1050	
1589	31957	B	1614	1	561	
1590	31958	B	1615	127	330	
1591	31959	C	1616	202	443	
1592	31960	B	1617	1	924	
1593	31961	C	1618	60	419	
1594	31962	C	1619	285	602	
1595	31963	C	1620	1	93	
1596	31964	B	1621	1	480	
1597	31965	B	1622	96	416	
1598	31966	B	1623	78	1581	
1599	31967	B	1624	1	2259	
1600	31968	C	1625	180	371	
1601	31969	B	1626	1	852	
1602	31970	B	1627	1	204	
1603	31971	B	1628	37	2613	
1604	31972	B	1629	66	1505	
1605	31973	B	1630	1	1792	
1606	31974	B	1631	100	522	
1607	31975	B	1632	252	2347	
1608	31976	C	1633	294	450	
1609	31977	C	1634	118	372	
1610	31978	B	1635	1	799	
1611	31979	B	1636	1	2496	
1612	31980	B	1637	100	1188	
1613	31981	B	1638	35	1654	
1614	31982	B	1639	46	783	
1615	31983	B	1640	8	1428	
1616	31984	B	1641	1	2121	
1617	31985	B	1642	92	667	
1618	31986	B	1643	1	339	
1619	31987	C	1644	79	434	
1620	31988	C	1645	592	921	
1621	31989	C	1646	1	171	
1622	31990	C	1647	76	264	
1623	31991	B	1648	157	912	
1624	31992	B	1649	10	462	
1625	31993	C	1650	10	333	
1626	31994	C	1651	763	1001	
1627	31995	B	1652	202	701	
1628	31996	C	1653	215	572	
1629	31997	B	1654	261	399	
1630	31998	C	1655	623	749	
1631	31999	B	1656	198	1524	
1632	32000	B	1657	108	575	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
1633	32001	B	1658	40	2173	
1634	32002	B	1659	1	479	
1635	32003	B	1660	1	1542	
1636	32004	B	1661	1	849	
1637	32005	B	1662	1	684	
1638	32006	B	1663	1	318	
1639	32007	B	1664	1	406	
1640	32008	B	1665	1	393	
1641	32009	B	1666	1	210	
1642	32010	B	1667	1	450	
1643	32011	B	1668	1	471	
1644	32012	B	1669	1	471	
1645	32013	B	1670	282	580	
1646	32014	B	1671	1	789	
1647	32015	B	1672	1	324	
1648	32016	B	1673	1	465	
1649	32017	B	1674	1	948	
1650	32018	C	1675	24	401	
1651	32019	B	1676	46	401	
1652	32020	B	1677	251	1041	
1653	32021	C	1678	1	177	
1654	32022	B	1679	1	189	
1655	32023	B	1680	65	769	
1656	32024	C	1681	1	564	
1657	32025	B	1682	65	769	
1658	32026	B	1683	1	1743	
1659	32027	B	1684	1	615	
1660	32028	B	1685	1	323	
1661	32029	B	1686	1	618	
1662	32030	B	1687	1	579	
1663	32031	C	1688	142	216	
1664	32032	C	1689	145	432	
1665	32033	B	1690	1	729	
1666	32034	C	1691	1	192	
1667	32035	C	1692	1	474	
1668	32036	B	1693	326	1662	
1669	32037	B	1694	50	1462	
1670	32038	C	1695	1	432	
1671	32039	B	1696	173	375	
1672	32040	B	1697	1	1917	
1673	32041	B	1698	57	365	
1674	32042	B	1699	78	1250	
1675	32043	B	1700	8	2210	
1676	32044	B	1701	1	474	
1677	32045	B	1702	47	879	
1678	32046	B	1703	1	465	
1679	32047	B	1704	65	473	
1680	32048	B	1705	89	1908	
1681	32049	C	1706	1	612	
1682	32050	C	1707	80	226	
1683	32051	B	1708	992	2023	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
1684	32052	B	1709	1293	1497	
1685	32053	B	1710	29	1480	
1686	32054	C	1711	1664	2179	
1687	32055	B	1712	183	8544	
1688	32056	C	1713	60	472	
1689	32057	B	1714	202	735	
1690	32058	B	1715	532	661	
1691	32059	B	1716	1	453	
1692	32060	B	1717	24	320	
1693	32061	B	1718	59	583	
1694	32062	B	1719	1	369	
1695	32063	B	1720	51	204	
1696	32064	B	1721	318	849	
1697	32065	B	1722	1	597	
1698	32066	B	1723	1	325	
1699	32067	B	1724	1	675	
1700	32068	B	1725	1	631	
1701	32069	B	1726	1	1017	
1702	32070	B	1727	158	727	
1703	32071	B	1728	296	798	
1704	32072	B	1729	1	1128	
1705	32073	C	1730	237	356	
1706	32074	C	1731	393	519	
1707	32075	B	1732	1	6432	
1708	32076	B	1733	124	402	
1709	32077	B	1734	35	421	
1710	32078	C	1735	203	385	
1711	32079	B	1736	16	406	
1712	32080	B	1737	21	306	
1713	32081	B	1738	97	352	
1714	32082	B	1739	64	7164	
1715	32083	B	1740	553	1197	
1716	32084	B	1741	553	720	
1717	32085	B	1742	1	4029	
1718	32086	B	1743	63	422	
1719	32087	B	1744	342	451	
1720	32088	B	1745	1	1238	
1721	32089	B	1746	1	2393	
1722	32090	B	1747	1667	1833	
1723	32091	C	1748	33	287	
1724	32092	B	1749	1	469	
1725	32093	B	1750	75	166	
1726	32094	B	1751	120	756	
1727	32095	C	1752	1	1098	
1728	32096	B	1753	1	486	
1729	32097	C	1754	25	374	
1730	32098	C	1755	149	394	
1731	32099	B	1756	1	660	
1732	32100	B	1757	26	391	
1733	32101	B	1758	282	419	
1734	32102	B	1759	132	717	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
1735	32103	B	1760	127	698	
1736	32104	B	1761	56	549	
1737	32105	B	1762	325	2681	
1738	32106	C	1763	465	893	
1739	32107	C	1764	123	764	
1740	32108	B	1765	206	402	
1741	32109	B	1766	393	900	
1742	32110	C	1767	1	360	
1743	32111	B	1768	285	482	
1744	32112	B	1769	1	405	
1745	32113	C	1770	304	399	
1746	32114	B	1771	1	273	
1747	32115	B	1772	67	1464	
1748	32116	B	1773	1	1122	
1749	32117	B	1774	1	1185	
1750	32118	B	1775	44	145	
1751	32119	B	1776	1	1050	
1752	32120	B	1777	250	762	
1753	32121	B	1778	1	390	
1754	32122	B	1779	172	867	
1755	32123	B	1780	327	637	
1756	32124	B	1781	1	1101	
1757	32125	C	1782	10	216	
1758	32126	B	1783	1	1449	
1759	32127	B	1784	1	402	
1760	32128	C	1785	134	418	
1761	32129	B	1786	1	417	
1762	32130	B	1787	1	384	
1763	32131	C	1788	1	738	
1764	32132	C	1789	68	280	
1765	32133	B	1790	101	327	
1766	32134	B	1791	1	1257	
1767	32135	C	1792	168	311	
1768	32136	B	1793	33	120	
1769	32137	C	1794	1	150	
1770	32138	C	1795	1	378	
1771	32139	C	1796	100	267	
1772	32140	C	1797	1	318	
1773	32141	C	1798	1	429	
1774	32142	C	1799	194	379	
1775	32143	B	1800	1	363	
1776	32144	B	1801	1	384	
1777	32145	B	1802	1	4462	
1778	32146	B	1803	235	425	
1779	32147	B	1804	8	1187	
1780	32148	B	1805	1	480	
1781	32149	B	1806	1	240	
1782	32150	B	1807	1	891	
1783	32151	C	1808	1	366	
1784	32152	B	1809	376	776	
1785	32153	B	1810	304	876	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
1786	32154	B	1811	1	939	
1787	32155	B	1812	4	744	
1788	32156	B	1813	1	717	
1789	32157	C	1814	67	366	
1790	32158	B	1815	185	847	
1791	32159	C	1816	1	315	
1792	32160	B	1817	87	297	
1793	32161	B	1818	1	1190	
1794	32162	B	1819	1	848	
1795	32163	B	1820	934	1158	
1796	32164	C	1821	1	477	
1797	32165	C	1822	6	125	
1798	32166	B	1823	335	536	
1799	32167	B	1824	157	324	
1800	32168	C	1825	176	361	
1801	32169	C	1826	1	120	
1802	32170	C	1827	25	360	
1803	32171	C	1828	246	377	
1804	32172	C	1829	4782	5015	
1805	32173	B	1830	1105	3034	
1806	32174	B	1831	818	874	
1807	32175	C	1832	1	444	
1808	32176	B	1833	589	734	
1809	32177	B	1834	1	264	
1810	32178	B	1835	46	112	
1811	32179	B	1836	1	360	
1812	32180	B	1837	589	734	
1813	32181	B	1838	1	675	
1814	32182	B	1839	1	1194	
1815	32183	B	1840	121	880	
1816	32184	B	1841	35	853	
1817	32185	B	1842	1	426	
1818	32186	C	1843	1	252	
1819	32187	B	1844	1	323	
1820	32188	B	1845	1	789	
1821	32189	C	1846	337	1521	
1822	32190	C	1847	1	345	
1823	32191	B	1848	331	3385	
1824	32192	B	1849	1	1584	
1825	32193	B	1850	1	957	
1826	32194	B	1851	226	1794	
1827	32195	B	1852	52	594	
1828	32196	C	1853	1	615	
1829	32197	B	1854	1	318	
1830	32198	B	1855	297	450	
1831	32199	C	1856	87	404	
1832	32200	C	1857	1	171	
1833	32201	C	1858	1	171	
1834	32202	B	1859	34	831	
1835	32203	B	1860	1	1375	
1836	32204	B	1861	1	546	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
1837	32205	C	1862	36	182	
1838	32206	B	1863	392	1043	
1839	32207	B	1864	1	1283	
1840	32208	C	1865	283	591	
1841	32209	C	1866	97	108	
1842	32210	C	1867	25	250	
1843	32211	C	1868	142	448	
1844	32212	C	1869	1	576	
1845	32213	C	1870	1	396	
1846	32214	B	1871	1	885	
1847	32215	C	1872	321	848	
1848	32216	B	1873	82	871	
1849	32217	C	1874	1	723	
1850	32218	C	1875	1	426	
1851	32219	C	1876	624	803	
1852	32220	B	1877	1	588	
1853	32221	B	1878	39	58	
1854	32222	B	1879	1	1011	
1855	32223	B	1880	1	654	
1856	32224	C	1881	1	498	
1857	32225	C	1882	1	249	
1858	32226	C	1883	507	785	
1859	32227	C	1885	310	404	
1860	32228	B	1886	448	618	
1861	32229	B	1887	1	388	
1862	32230	B	1888	106	414	
1863	32231	B	1889	82	4206	
1864	32232	B	1890	1	240	
1865	32233	B	1891	1	324	
1866	32234	C	1892	243	447	
1867	32235	C	1893	139	228	
1868	32236	C	1894	61	300	
1869	32237	C	1895	271	429	
1870	32238	B	1896	545	1054	
1871	32239	B	1897	609	706	
1872	32240	B	1898	1	2521	
1873	32241	C	1899	152	517	
1874	32242	B	1900	217	313	
1875	32243	C	1901	86	193	
1876	32244	C	1902	29	271	
1877	32245	B	1903	1	522	
1878	32246	C	1904	37	225	
1879	32247	C	1905	84	308	
1880	32248	B	1906	36	1569	
1881	32249	B	1907	1	522	
1882	32250	C	1908	1	510	
1883	32251	B	1909	1	936	
1884	32252	C	1910	1	162	
1885	32253	C	1911	155	427	
1886	32254	B	1912	1	1282	
1887	32255	B	1913	165	270	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
1888	32256	B	1914	513	9470	
1889	32257	B	1915	35	871	
1890	32258	B	1916	1	690	
1891	32259	C	1917	86	271	
1892	32260	B	1918	1	690	
1893	32261	C	1919	14	301	
1894	32262	B	1920	1	936	
1895	32263	B	1921	1	1901	
1896	32264	B	1922	36	238	
1897	32265	B	1923	1	738	
1898	32266	C	1924	5	364	
1899	32267	C	1925	43	494	
1900	32268	C	1926	96	263	
1901	32269	B	1927	1	207	
1902	32270	B	1928	1	290	
1903	32271	B	1929	52	482	
1904	32272	B	1930	271	408	
1905	32273	B	1931	114	309	
1906	32274	C	1932	218	398	
1907	32275	B	1933	1	1011	
1908	32276	B	1934	1	702	
1909	32277	B	1935	1	1305	
1910	32278	C	1936	141	374	
1911	32279	B	1937	1	834	
1912	32280	B	1938	47	363	
1913	32281	B	1939	73	558	
1914	32282	B	1940	373	864	
1915	32283	B	1941	96	377	
1916	32284	B	1942	55	2711	
1917	32285	B	1945	833	1352	
1918	32286	B	1946	1	1101	
1919	32287	B	1947	865	1070	
1920	32288	C	1948	1	285	
1921	32289	B	1949	1	642	
1922	32290	B	1950	124	813	
1923	32291	B	1951	1	654	
1924	32292	B	1952	180	303	
1925	32293	C	1953	15	170	
1926	32294	B	1954	245	646	
1927	32295	B	1955	100	824	
1928	32296	C	1956	52	348	
1929	32297	B	1957	1	678	
1930	32298	B	1958	1	954	
1931	32299	B	1959	1	675	
1932	32300	C	1960	52	348	
1933	32301	B	1961	71	251	
1934	32302	B	1962	427	747	
1935	32303	B	1963	1	453	
1936	32304	B	1964	1	375	
1937	32305	B	1965	117	1109	
1938	32306	C	1966	47	133	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
1939	32307	B	1967	79	1149	
1940	32308	B	1968	1	693	
1941	32309	B	1969	1	1179	
1942	32310	B	1970	1	639	
1943	32311	B	1971	502	1294	
1944	32312	C	1972	670	1185	
1945	32313	B	1973	1	1044	
1946	32314	B	1974	1	3645	
1947	32315	B	1975	1	2877	
1948	32316	B	1976	1	1579	
1949	32317	B	1977	1	750	
1950	32318	B	1978	1	438	
1951	32319	C	1979	122	307	
1952	32320	C	1980	71	271	
1953	32321	C	1981	151	363	
1954	32322	C	1982	122	307	
1955	32323	C	1983	55	282	
1956	32324	C	1984	89	385	
1957	32325	C	1985	48	275	
1958	32326	C	1986	246	557	
1959	32327	B	1987	394	2565	
1960	32328	B	1988	1	432	
1961	32329	B	1989	46	483	
1962	32330	B	1990	150	482	
1963	32331	B	1991	10	265	
1964	32332	C	1992	40	162	
1965	32333	B	1993	1	3639	
1966	32334	B	1994	83	179	
1967	32335	B	1995	39	1452	
1968	32336	B	1996	50	384	
1969	32337	B	1997	256	351	
1970	32338	B	1998	1	771	
1971	32339	B	1999	1	489	
1972	32340	B	2000	37	447	
1973	32341	B	2001	1	1272	
1974	32342	B	2002	1	2559	
1975	32343	C	2003	221	589	
1976	32344	C	2004	415	1033	
1977	32345	B	2007	318	694	
1978	32346	B	2008	31	819	
1979	32347	B	2009	1	276	
1980	32348	B	2010	1	369	
1981	32349	B	2011	85	628	
1982	32350	B	2012	19	178	
1983	32351	B	2013	217	393	
1984	32352	B	2014	1	779	
1985	32353	B	2015	107	650	
1986	32354	B	2016	313	527	
1987	32355	B	2017	32	258	
1988	32356	C	2018	51	345	
1989	32357	B	2019	1	393	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
1990	32358	B	2020	647	1362	
1991	32359	C	2021	16	378	
1992	32360	B	2022	32	349	
1993	32361	C	2023	256	425	
1994	32362	C	2024	134	382	
1995	32363	B	2025	138	171	
1996	32364	B	2026	1	1626	
1997	32365	B	2027	509	810	
1998	32366	C	2028	1	513	
1999	32367	C	2029	7	375	
2000	32368	C	2030	1	410	
2001	32369	B	2031	1	864	
2002	32370	B	2032	110	928	
2003	32371	B	2033	1	1026	
2004	32372	B	2034	1	1008	
2005	32373	B	2035	1	588	
2006	32374	B	2036	1	412	
2007	32375	B	2037	1	1851	
2008	32376	B	2038	309	663	
2009	32377	B	2039	1	525	
2010	32378	B	2040	1	2214	
2011	32379	B	2041	1	486	
2012	32380	B	2042	1	774	
2013	32381	B	2043	1	596	
2014	32382	B	2044	305	395	
2015	32383	C	2045	27	185	
2016	32384	B	2046	1	1071	
2017	32385	B	2047	1	1326	
2018	32386	B	2048	1	3761	
2019	32387	C	2049	55	189	
2020	32388	B	2050	1016	1683	
2021	32389	C	2051	942	1130	
2022	32390	B	2052	1	598	
2023	32391	B	2053	1	768	
2024	32392	B	2054	1	999	
2025	32393	C	2055	1	252	
2026	32394	B	2056	154	606	
2027	32395	B	2057	1	846	
2028	32396	C	2058	334	690	
2029	32397	B	2059	268	5712	
2030	32398	C	2060	117	662	
2031	32399	B	2061	1	3504	
2032	32400	B	2062	816	927	
2033	32401	B	2063	1	342	
2034	32402	B	2064	1	1443	
2035	32403	C	2065	53	102	
2036	32404	C	2066	271	528	
2037	32405	B	2067	1	843	
2038	32406	C	2068	187	408	
2039	32407	C	2069	174	320	
2040	32408	B	2070	31	534	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
2041	32409	C	2071	183	329	
2042	32410	B	2072	3	389	
2043	32411	B	2073	78	974	
2044	32412	B	2074	467	692	
2045	32413	C	2075	605	965	
2046	32414	B	2076	1	555	
2047	32415	B	2077	1	390	
2048	32416	B	2078	1	2522	
2049	32417	B	2079	24	94	
2050	32418	B	2080	78	593	
2051	32419	B	2081	1	612	
2052	32420	B	2082	42	342	
2053	32421	B	2083	1	477	
2054	32422	B	2084	57	1640	
2055	32423	C	2085	110	307	
2056	32424	B	2086	1	591	
2057	32425	C	2087	14	355	
2058	32426	B	2088	47	998	
2059	32427	B	2089	1	498	
2060	32428	C	2090	357	560	
2061	32429	B	2091	1	522	
2062	32430	C	2092	231	659	
2063	32431	C	2093	36	167	
2064	32432	B	2094	394	2695	
2065	32433	B	2096	61	2215	
2066	32434	B	2097	204	572	
2067	32435	C	2098	476	652	
2068	32436	B	2099	1	190	
2069	32437	C	2100	1	259	
2070	32438	B	2101	1	2625	
2071	32439	B	2102	1403	2950	
2072	32440	B	2103	672	1955	
2073	32441	C	2104	1	351	
2074	32442	B	2105	1	567	
2075	32443	C	2106	176	304	
2076	32444	C	2107	27	308	
2077	32445	C	2108	68	307	
2078	32446	C	2109	322	567	
2079	32447	B	2110	1	1297	
2080	32448	B	2111	281	1488	
2081	32449	B	2112	12	2497	
2082	32450	C	2113	90	284	
2083	32451	B	2114	1	2466	
2084	32452	B	2115	1	603	
2085	32453	B	2116	1	954	
2086	32454	B	2117	205	441	
2087	32455	B	2118	68	2052	
2088	32456	B	2119	271	639	
2089	32457	B	2120	1	1356	
2090	32458	B	2121	247	1326	
2091	32459	B	2122	1	1041	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
2092	32460	B	2123	1	1695	
2093	32461	B	2124	1	1767	
2094	32462	B	2125	1	2286	
2095	32463	B	2126	1	1167	
2096	32464	B	2127	1	2343	
2097	32465	B	2128	1	1056	
2098	32466	B	2129	1	1379	
2099	32467	B	2130	1	1839	
2100	32468	B	2131	1	5460	
2101	32469	B	2132	133	549	
2102	32470	B	2133	1	534	
2103	32471	B	2134	1	537	
2104	32472	B	2135	1	49	
2105	32473	C	2136	1	432	
2106	32474	B	2137	1	615	
2107	32475	B	2138	146	556	
2108	32476	B	2139	133	1434	
2109	32477	B	2140	1	357	
2110	32478	C	2141	1	429	
2111	32479	B	2142	1	411	
2112	32480	B	2143	1	459	
2113	32481	C	2144	224	550	
2114	32482	B	2145	1	1035	
2115	32483	B	2146	1	342	
2116	32484	C	2147	1	321	
2117	32485	C	2148	1	317	
2118	32486	B	2149	1	495	
2119	32487	B	2150	146	556	
2120	32488	C	2151	1	390	
2121	32489	C	2152	461	643	
2122	32490	C	2153	198	416	
2123	32491	C	2154	258	500	
2124	32492	B	2155	291	1034	
2125	32493	B	2156	1	834	
2126	32494	B	2157	1	7852	
2127	32495	B	2158	1	1320	
2128	32496	B	2159	1631	1756	
2129	32497	B	2160	500	8643	
2130	32498	C	2161	193	475	
2131	32499	B	2162	1	795	
2132	32500	B	2163	1	663	
2133	32501	C	2164	1	303	
2134	32502	B	2165	266	385	
2135	32503	B	2166	1	704	
2136	32504	B	2167	1	720	
2137	32505	B	2168	364	507	
2138	32506	B	2169	44	197	
2139	32507	C	2170	72	224	
2140	32508	C	2171	228	393	
2141	32509	C	2172	241	396	
2142	32510	C	2173	415	552	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
2143	32511	B	2174	64	268	
2144	32512	C	2175	1	462	
2145	32513	C	2176	1	357	
2146	32514	B	2177	1	3213	
2147	32515	B	2178	119	682	
2148	32516	B	2179	1	405	
2149	32517	B	2180	297	769	
2150	32518	B	2181	1	1314	
2151	32519	C	2182	156	287	
2152	32520	B	2183	1	756	
2153	32521	B	2184	1	645	
2154	32522	B	2185	1	948	
2155	32523	B	2186	1	660	
2156	32524	B	2187	186	518	
2157	32525	B	2188	1	3570	
2158	32526	B	2189	1	3354	
2159	32527	B	2190	1	2232	
2160	32528	B	2191	1	1356	
2161	32529	B	2192	1	1103	
2162	32530	B	2193	1	1902	
2163	32531	B	2194	1	2232	
2164	32532	B	2195	1	2991	
2165	32533	B	2196	1	2136	
2166	32534	B	2197	1	1524	
2167	32535	B	2198	1	2106	
2168	32536	B	2199	1	1224	
2169	32537	B	2200	1	1935	
2170	32538	B	2201	1	1428	
2171	32539	B	2202	1	858	
2172	32540	B	2203	1	2162	
2173	32541	B	2204	1	1374	
2174	32542	B	2205	205	3666	
2175	32543	B	2206	59	4311	
2176	32544	B	2207	1	1311	
2177	32545	B	2208	1	2742	
2178	32546	B	2209	1	1878	
2179	32547	B	2210	1	1074	
2180	32548	B	2211	1	2217	
2181	32549	B	2212	1	1945	
2182	32550	B	2213	1	1941	
2183	32551	B	2214	1	1737	
2184	32552	B	2215	1	1422	
2185	32553	B	2216	22	9087	
2186	32554	B	2217	1	4954	
2187	32555	B	2218	1	1812	
2188	32556	B	2219	1	939	
2189	32557	B	2220	1	2895	
2190	32558	B	2221	1	6223	
2191	32559	B	2222	109	4966	
2192	32560	B	2223	3807	9479	
2193	32561	B	2224	1	4903	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
2194	32562	B	2225	210	516	
2195	32563	C	2226	185	292	
2196	32564	B	2227	1	657	
2197	32565	B	2228	1	1011	
2198	32566	B	2229	1	1303	
2199	32567	C	2230	69	182	
2200	32568	B	2231	1	321	
2201	32569	B	2232	88	522	
2202	32570	B	2233	527	1207	
2203	32571	B	2234	118	375	
2204	32572	B	2235	8	148	
2205	32573	B	2236	609	1121	
2206	32574	B	2237	1	1500	
2207	32575	C	2238	121	330	
2208	32576	B	2239	1	591	
2209	32577	B	2240	125	471	
2210	32578	B	2241	64	909	
2211	32579	B	2242	13	579	
2212	32580	B	2243	249	531	
2213	32581	C	2244	107	928	
2214	32582	B	2245	213	322	
2215	32583	C	2246	373	441	
2216	32584	B	2247	54	2723	
2217	32585	B	2248	94	529	
2218	32586	B	2249	57	260	
2219	32587	B	2250	674	1972	
2220	32588	B	2251	1	1053	
2221	32589	C	2252	186	347	
2222	32590	B	2253	26	193	
2223	32591	B	2254	1	5442	
2224	32592	B	2255	428	3792	
2225	32593	B	2256	9	199	
2226	32594	B	2257	421	2932	
2227	32595	B	2258	305	547	
2228	32596	B	2259	1	891	
2229	32597	B	2260	1	641	
2230	32598	B	2261	108	542	
2231	32599	B	2262	105	440	
2232	32600	B	2263	553	729	
2233	32601	B	2264	1	645	
2234	32602	B	2265	291	452	
2235	32603	B	2266	143	348	
2236	32604	C	2267	310	426	
2237	32605	B	2268	1	1344	
2238	32606	B	2269	237	2834	
2239	32607	B	2270	1	2922	
2240	32608	B	2271	109	3499	
2241	32609	B	2272	1	1611	
2242	32610	B	2273	1	1575	
2243	32611	B	2274	1	1314	
2244	32612	B	2275	1	1209	

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2245	32613	B	2276	1	2022	
2246	32614	B	2277	1	1938	
2247	32615	B	2279	1	1806	
2248	32616	B	2280	1	2361	
2249	32617	B	2281	1	2732	
2250	32618	B	2282	1	3703	
2251	32619	C	2283	1	507	
2252	32620	B	2284	118	316	
2253	32621	B	2285	1	272	
2254	32622	B	2286	37	388	
2255	32623	B	2287	1	660	
2256	32624	B	2288	431	633	
2257	32625	B	2289	1	1032	
2258	32626	B	2290	1	1227	
2259	32627	C	2291	27	296	
2260	32628	B	2292	58	370	
2261	32629	B	2293	1	1275	
2262	32630	B	2294	1	1299	
2263	32631	C	2295	227	613	
2264	32632	B	2296	1	297	
2265	32633	B	2297	126	206	
2266	32634	C	2298	1	387	
2267	32635	B	2299	19	279	
2268	32636	B	2300	1	612	
2269	32637	C	2301	81	191	
2270	32638	B	2302	120	308	
2271	32639	B	2303	1	2145	
2272	32640	C	2304	270	416	
2273	32641	B	2305	31	627	
2274	32642	B	2306	128	499	
2275	32643	B	2307	61	388	
2276	32644	B	2308	744	2094	
2277	32645	B	2309	241	669	
2278	32646	B	2310	1	285	
2279	32647	B	2311	137	307	
2280	32648	C	2312	168	362	
2281	32649	C	2313	8	394	
2282	32650	B	2314	1	489	
2283	32651	C	2315	1	204	
2284	32652	B	2316	1	2361	
2285	32653	B	2317	1	2265	
2286	32654	B	2318	1	2268	
2287	32655	B	2319	1	2337	
2288	32656	B	2320	1	2196	
2289	32657	B	2321	1	2298	
2290	32658	B	2322	1	2880	
2291	32659	B	2323	1	2562	
2292	32660	B	2324	1	2835	
2293	32661	B	2325	1	2172	
2294	32662	B	2326	675	2515	
2295	32663	B	2327	1	2709	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
2296	32664	B	2328	1	2478	
2297	32665	B	2329	1	2748	
2298	32666	B	2330	877	4763	
2299	32667	B	2331	1	2590	
2300	32668	B	2332	1	597	
2301	32669	C	2333	279	412	
2302	32670	C	2334	507	878	
2303	32671	C	2335	1	147	
2304	32672	B	2336	52	573	
2305	32673	C	2337	211	446	
2306	32674	B	2338	1	1669	
2307	32675	B	2339	69	418	
2308	32676	B	2340	1	2778	
2309	32677	B	2341	1	1896	
2310	32678	B	2342	1	1836	
2311	32679	B	2343	1	2463	
2312	32680	B	2344	287	1785	
2313	32681	B	2345	1	2860	
2314	32682	B	2346	1	1281	
2315	32683	B	2347	1	1176	
2316	32684	B	2348	1	1431	
2317	32685	B	2349	1	2361	
2318	32686	B	2350	592	1815	
2319	32687	B	2351	1	2764	
2320	32688	C	2352	309	581	
2321	32689	B	2353	99	5619	
2322	32690	B	2354	133	3213	
2323	32691	B	2355	1	3193	
2324	32692	B	2356	1	3291	
2325	32693	B	2357	1	4019	
2326	32694	B	2358	167	4093	
2327	32695	B	2359	1	3534	
2328	32696	B	2360	1	3405	
2329	32697	B	2361	1	3555	
2330	32698	B	2362	1	3786	
2331	32699	B	2363	1	3414	
2332	32700	B	2364	1	5130	
2333	32701	B	2365	1	8244	
2334	32702	B	2366	1	7995	
2335	32703	B	2367	1	1980	
2336	32704	B	2368	1	4269	
2337	32705	B	2369	1	169	
2338	32706	B	2370	1	573	
2339	32707	B	2371	388	1101	
2340	32708	C	2372	1	354	
2341	32709	B	2373	134	1057	
2342	32710	B	2374	91	1464	
2343	32711	B	2375	117	767	
2344	32712	B	2376	1	486	
2345	32713	C	2377	1	726	
2346	32714	C	2378	31	447	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
2347	32715	B	2379	1	402	
2348	32716	B	2380	22	427	
2349	32717	B	2381	351	560	
2350	32718	B	2382	1	1122	
2351	32719	B	2383	1	1035	
2352	32720	B	2384	1	309	
2353	32721	B	2385	80	673	
2354	32722	B	2386	160	659	
2355	32723	B	2387	1	858	
2356	32724	C	2388	228	365	
2357	32725	B	2389	1	531	
2358	32726	B	2390	218	670	
2359	32727	C	2391	182	484	
2360	32728	C	2392	1	738	
2361	32729	C	2393	27	316	
2362	32730	B	2394	291	498	
2363	32731	C	2395	230	409	
2364	32732	B	2396	228	1361	
2365	32733	C	2397	210	548	
2366	32734	B	2398	309	1202	
2367	32735	C	2399	100	406	
2368	32736	B	2400	440	2579	
2369	32737	C	2401	102	359	
2370	32738	B	2402	1	414	
2371	32739	B	2403	717	976	
2372	32740	B	2404	1	777	
2373	32741	B	2405	1	208	
2374	32742	B	2406	1	570	
2375	32743	B	2407	187	525	
2376	32744	B	2408	20	499	
2377	32745	B	2409	1	210	
2378	32746	B	2410	41	166	
2379	32747	B	2411	29	348	
2380	32748	B	2412	1	564	
2381	32749	C	2413	250	366	
2382	32750	B	2414	164	430	
2383	32751	C	2415	141	340	
2384	32752	B	2416	304	422	
2385	32753	B	2417	1	2031	
2386	32754	B	2418	1	1527	
2387	32755	B	2419	1	2892	
2388	32756	B	2420	218	4186	
2389	32757	B	2421	203	655	
2390	32758	C	2422	1	346	
2391	32759	B	2423	299	433	
2392	32760	B	2424	172	525	
2393	32761	B	2425	1	3270	
2394	32762	B	2426	202	481	
2395	32763	B	2427	148	3473	
2396	32764	C	2428	182	460	
2397	32765	B	2429	116	2953	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
2398	32766	B	2430	153	332	
2399	32767	B	2431	267	2752	
2400	32768	B	2432	1	848	
2401	32769	C	2433	54	350	
2402	32770	B	2434	160	531	
2403	32771	B	2435	159	184	
2404	32772	B	2436	44	293	
2405	32773	C	2437	129	438	
2406	32774	C	2438	255	469	
2407	32775	B	2439	292	456	
2408	32776	B	2440	86	225	
2409	32777	B	2441	1	603	
2410	32778	B	2442	305	402	
2411	32779	C	2443	117	332	
2412	32780	B	2444	1	642	
2413	32781	B	2445	50	238	
2414	32782	B	2446	350	1331	
2415	32783	B	2447	1	867	
2416	32784	B	2448	1	498	
2417	32785	B	2449	40	849	
2418	32786	B	2450	187	404	
2419	32787	B	2451	1	921	
2420	32788	B	2452	439	517	
2421	32789	C	2453	143	682	
2422	32790	B	2454	87	401	
2423	32791	B	2455	44	277	
2424	32792	B	2456	1	639	
2425	32793	B	2457	1	816	
2426	32794	B	2458	100	454	
2427	32795	C	2459	717	923	
2428	32796	C	2460	1	412	
2429	32797	C	2461	80	394	
2430	32798	B	2462	278	323	
2431	32799	C	2463	9	239	
2432	32800	B	2464	1	537	
2433	32801	B	2465	1	798	
2434	32802	B	2466	1	861	
2435	32803	B	2467	611	979	
2436	32804	B	2468	56	166	
2437	32805	C	2469	40	495	
2438	32806	B	2470	1	216	
2439	32807	B	2471	273	385	
2440	32808	B	2472	77	489	
2441	32809	C	2473	480	791	
2442	32810	B	2474	110	1318	
2443	32811	B	2475	114	563	
2444	32812	B	2476	813	3193	
2445	32813	C	2477	198	650	
2446	32814	B	2478	1	234	
2447	32815	B	2479	7	174	
2448	32816	B	2480	1	1035	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
2449	32817	B	2481	1	564	
2450	32818	B	2482	16	894	
2451	32819	B	2483	1	207	
2452	32820	B	2484	1	2742	
2453	32821	B	2485	1	1071	
2454	32822	B	2486	58	1228	
2455	32823	C	2487	51	179	
2456	32824	B	2488	1	1119	
2457	32825	C	2489	147	398	
2458	32826	C	2490	1	504	
2459	32827	C	2491	4	240	
2460	32828	B	2492	190	388	
2461	32829	B	2493	1	594	
2462	32830	C	2494	299	477	
2463	32831	B	2495	1	2328	
2464	32832	C	2496	1	924	
2465	32833	B	2497	1	2703	
2466	32834	B	2498	504	1392	
2467	32835	C	2499	649	1239	
2468	32836	B	2500	46	842	
2469	32837	B	2501	251	555	
2470	32838	B	2502	258	326	
2471	32839	B	2503	49	386	
2472	32840	C	2504	63	383	
2473	32841	B	2505	150	585	
2474	32842	B	2506	65	678	
2475	32843	C	2507	477	634	
2476	32844	B	2508	80	337	
2477	32845	B	2509	1	1233	
2478	32846	B	2510	1	2526	
2479	32847	B	2511	192	2617	
2480	32848	B	2512	1	921	
2481	32849	B	2513	1	1650	
2482	32850	B	2514	79	1587	
2483	32851	B	2515	1	657	
2484	32852	B	2516	1	1260	
2485	32853	B	2517	1	762	
2486	32854	C	2518	1	729	
2487	32855	B	2519	1	1299	
2488	32856	B	2520	1	882	
2489	32857	C	2521	1	369	
2490	32858	B	2522	52	573	
2491	32859	B	2523	1	570	
2492	32860	B	2524	1	2376	
2493	32861	B	2525	1	786	
2494	32862	B	2526	1	760	
2495	32863	B	2527	73	714	
2496	32864	B	2528	1	2976	
2497	32865	B	2529	1	1021	
2498	32866	B	2530	1	1386	
2499	32867	B	2531	352	1239	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
2500	32868	B	2532	1	1740	
2501	32869	B	2533	1	915	
2502	32870	B	2534	392	1393	
2503	32871	B	2535	1	4868	
2504	32872	B	2536	1	2667	
2505	32873	B	2537	1	825	
2506	32874	B	2538	1	735	
2507	32875	B	2539	88	469	
2508	32876	C	2540	1	390	
2509	32877	C	2541	113	328	
2510	32878	B	2542	475	848	
2511	32879	B	2543	472	1482	
2512	32880	C	2544	42	593	
2513	32881	B	2545	470	998	
2514	32882	B	2546	83	339	
2515	32883	B	2547	1	501	
2516	32884	B	2548	1198	1432	
2517	32885	B	2549	1	486	
2518	32886	B	2550	454	1626	
2519	32887	C	2551	227	388	
2520	32888	B	2552	25	687	
2521	32889	B	2553	569	753	
2522	32890	C	2554	147	384	
2523	32891	B	2555	210	419	
2524	32892	B	2556	1	1185	
2525	32893	C	2557	93	257	
2526	32894	C	2558	41	375	
2527	32895	C	2559	155	579	
2528	32896	B	2560	1	375	
2529	32897	C	2561	37	351	
2530	32898	C	2562	39	518	
2531	32899	B	2563	310	493	
2532	32900	C	2564	83	373	
2533	32901	B	2565	120	843	
2534	32902	C	2566	327	468	
2535	32903	B	2567	1	732	
2536	32904	C	2568	243	434	
2537	32905	C	2569	117	347	
2538	32906	C	2570	1	363	
2539	32907	C	2571	1	219	
2540	32908	B	2572	82	390	
2541	32909	B	2573	1152	1737	
2542	32910	C	2574	294	524	
2543	32911	B	2575	1	345	
2544	32912	B	2576	106	1073	
2545	32913	B	2577	1	313	
2546	32914	C	2578	1	594	
2547	32915	C	2579	16	102	
2548	32916	C	2580	1	441	
2549	32917	B	2581	1	462	
2550	32918	B	2582	113	1257	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
2551	32919	B	2583	1	402	
2552	32920	B	2584	489	570	
2553	32921	B	2585	218	356	
2554	32922	C	2586	225	345	
2555	32923	C	2587	472	621	
2556	32924	B	2588	1	984	
2557	32925	B	2589	1	1119	
2558	32926	B	2590	1	771	
2559	32927	B	2591	97	681	
2560	32928	B	2592	112	202	
2561	32929	C	2593	1	381	
2562	32930	C	2594	115	321	
2563	32931	C	2595	3	200	
2564	32932	B	2596	212	303	
2565	32933	C	2597	236	396	
2566	32934	B	2598	119	625	
2567	32935	C	2599	68	334	
2568	32936	C	2600	85	351	
2569	32937	B	2601	1	723	
2570	32938	C	2602	235	463	
2571	32939	B	2603	1	498	
2572	32940	C	2604	179	346	
2573	32941	B	2605	21	486	
2574	32942	B	2606	20	600	
2575	32943	B	2607	172	294	
2576	32944	B	2608	130	1200	
2577	32945	B	2609	61	243	
2578	32946	B	2610	1	753	
2579	32947	B	2611	1	2274	
2580	32948	B	2612	1	1848	
2581	32949	B	2613	1	1263	
2582	32950	B	2614	412	654	
2583	32951	C	2615	176	658	
2584	32952	B	2616	310	628	
2585	32953	B	2617	1	579	
2586	32954	C	2618	145	309	
2587	32955	B	2619	298	353	
2588	32956	B	2620	163	594	
2589	32957	B	2621	1	468	
2590	32958	B	2622	1	552	
2591	32959	B	2623	1	876	
2592	32960	B	2624	140	1333	
2593	32961	C	2625	1	222	
2594	32962	B	2626	1	645	
2595	32963	C	2627	49	339	
2596	32964	B	2628	1	1944	
2597	32965	C	2629	79	189	
2598	32966	C	2630	513	767	
2599	32967	B	2631	114	230	
2600	32968	B	2632	24	629	
2601	32969	B	2633	98	230	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
2602	32970	B	2634	99	462	
2603	32971	B	2635	127	1498	
2604	32972	B	2636	22	105	
2605	32973	B	2637	1	1173	
2606	32974	B	2638	403	660	
2607	32975	B	2639	58	507	
2608	32976	C	2640	103	480	
2609	32977	B	2641	1	657	
2610	32978	B	2642	1	508	
2611	32979	B	2643	1	999	
2612	32980	C	2644	1	756	
2613	32981	C	2645	1	675	
2614	32982	B	2646	1	810	
2615	32983	B	2647	1	334	
2616	32984	B	2648	1	781	
2617	32985	B	2649	76	211	
2618	32986	B	2650	1	687	
2619	32987	B	2651	1	753	
2620	32988	B	2652	37	1038	
2621	32989	B	2653	1	456	
2622	32990	B	2654	1	168	
2623	32991	B	2655	1	786	
2624	32992	C	2656	571	1278	
2625	32993	C	2657	96	548	
2626	32994	C	2658	391	504	
2627	32995	B	2659	1	183	
2628	32996	C	2660	1	381	
2629	32997	B	2661	1	642	
2630	32998	B	2662	1	1164	
2631	32999	B	2663	1	471	
2632	33000	B	2664	1	972	
2633	33001	C	2665	75	182	
2634	33002	C	2666	125	226	
2635	33003	B	2667	1	462	
2636	33004	B	2668	1	422	
2637	33005	B	2669	81	616	
2638	33006	B	2670	197	713	
2639	33007	B	2671	1	882	
2640	33008	B	2672	1	507	
2641	33009	C	2673	176	274	
2642	33010	B	2674	250	446	
2643	33011	B	2675	19	118	
2644	33012	B	2676	21	120	
2645	33013	B	2677	373	389	
2646	33014	B	2678	1	1452	
2647	33015	B	2679	70	148	
2648	33016	C	2680	7	96	
2649	33017	C	2681	360	550	
2650	33018	B	2682	55	1618	
2651	33019	B	2683	1	309	
2652	33020	B	2684	100	528	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
2653	33021	B	2685	1	1191	
2654	33022	B	2686	52	834	
2655	33023	B	2687	1	933	
2656	33024	C	2688	80	322	
2657	33025	B	2689	127	415	
2658	33026	B	2690	74	190	
2659	33027	B	2691	150	380	
2660	33028	B	2692	1	1098	
2661	33029	C	2693	185	502	
2662	33030	B	2694	1	180	
2663	33031	C	2695	257	498	
2664	33032	B	2696	88	409	
2665	33033	C	2697	720	902	
2666	33034	C	2698	201	437	
2667	33035	C	2699	16	189	
2668	33036	B	2701	1	2286	
2669	33037	B	2702	1	1026	
2670	33038	B	2703	777	1035	
2671	33039	B	2704	1	1200	
2672	33040	B	2705	332	462	
2673	33041	B	2706	351	480	
2674	33042	B	2707	10	327	
2675	33043	B	2708	108	1325	
2676	33044	B	2709	36	189	
2677	33045	B	2710	54	3192	
2678	33046	B	2711	1	3423	
2679	33047	C	2712	5	280	
2680	33048	C	2713	1	88	
2681	33049	C	2714	1	153	
2682	33050	B	2715	70	231	
2683	33051	B	2716	11	427	
2684	33052	B	2717	74	943	
2685	33053	C	2718	109	315	
2686	33054	B	2719	1	335	
2687	33055	B	2720	108	506	
2688	33056	C	2721	1	486	
2689	33057	C	2722	87	441	
2690	33058	C	2723	85	276	
2691	33059	C	2724	86	280	
2692	33060	C	2725	108	254	
2693	33061	B	2726	1	930	
2694	33062	B	2727	23	847	
2695	33063	B	2728	19	182	
2696	33064	C	2729	190	300	
2697	33065	B	2730	67	650	
2698	33066	B	2731	1	1149	
2699	33067	B	2732	1	263	
2700	33068	B	2733	73	676	
2701	33069	B	2734	1	414	
2702	33070	B	2735	4	256	
2703	33071	B	2736	29	493	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
2704	33072	B	2737	1	1323	
2705	33073	B	2738	1	4209	
2706	33074	B	2739	538	728	
2707	33075	B	2740	344	1447	
2708	33076	C	2741	223	477	
2709	33077	B	2742	1	1091	
2710	33078	B	2743	1	2865	
2711	33079	B	2744	1	1203	
2712	33080	C	2745	120	401	
2713	33081	B	2746	1	688	
2714	33082	B	2747	1	549	
2715	33083	B	2748	196	1647	
2716	33084	B	2749	1	378	
2717	33085	C	2750	2	166	
2718	33086	B	2751	1	807	
2719	33087	C	2752	343	532	
2720	33088	B	2753	1	885	
2721	33089	C	2754	32	247	
2722	33090	B	2755	1	1152	
2723	33091	B	2756	1	885	
2724	33092	B	2757	87	359	
2725	33093	B	2758	71	418	
2726	33094	B	2759	117	1983	
2727	33095	B	2760	176	1045	
2728	33096	B	2761	25	187	
2729	33097	B	2762	1	315	
2730	33098	B	2763	1	351	
2731	33099	B	2764	1	396	
2732	33100	B	2765	12	350	
2733	33101	B	2766	1	411	
2734	33102	B	2767	1	1020	
2735	33103	B	2768	72	359	
2736	33104	B	2769	1	526	
2737	33105	B	2770	1	1233	
2738	33106	B	2771	1	1563	
2739	33107	B	2772	1	246	
2740	33108	B	2773	1	747	
2741	33109	B	2774	1	861	
2742	33110	C	2775	1	1278	
2743	33111	B	2776	1	630	
2744	33112	C	2777	22	147	
2745	33113	B	2778	242	744	
2746	33114	B	2779	54	178	
2747	33115	B	2780	1	2277	
2748	33116	B	2781	1	204	
2749	33117	B	2782	1	447	
2750	33118	B	2783	1	819	
2751	33119	B	2784	1	720	
2752	33120	B	2785	1	444	
2753	33121	B	2786	1	519	
2754	33122	B	2787	1	864	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
2755	33123	B	2788	1	654	
2756	33124	B	2789	1	772	
2757	33125	B	2790	1	930	
2758	33126	B	2791	1	3594	
2759	33127	B	2792	1	654	
2760	33128	B	2793	1	444	
2761	33129	B	2794	403	1560	
2762	33130	B	2795	1412	1495	
2763	33131	B	2796	536	2770	
2764	33132	B	2797	417	1025	
2765	33133	B	2798	108	326	
2766	33134	B	2799	1	694	
2767	33135	B	2800	380	541	
2768	33136	B	2801	1	916	
2769	33137	B	2802	509	1643	
2770	33138	C	2803	40	180	
2771	33139	B	2804	1	345	
2772	33140	C	2805	170	361	
2773	33141	C	2806	1	312	
2774	33142	C	2807	307	450	
2775	33143	B	2808	1	993	
2776	33144	B	2809	1	321	
2777	33145	B	2810	1	321	
2778	33146	C	2811	604	779	
2779	33147	B	2812	52	646	
2780	33148	C	2813	7	177	
2781	33149	C	2814	118	294	
2782	33150	B	2815	337	1512	
2783	33151	B	2816	32	335	
2784	33152	B	2817	1	1026	
2785	33153	C	2818	1	1044	
2786	33154	B	2819	1	1575	
2787	33155	B	2820	1	1356	
2788	33156	B	2821	1	3726	
2789	33157	B	2822	158	627	
2790	33158	B	2823	814	3116	
2791	33159	B	2824	1	2667	
2792	33160	B	2825	1	2778	
2793	33161	B	2826	96	662	
2794	33162	C	2827	163	245	
2795	33163	B	2828	1	381	
2796	33164	B	2829	47	378	
2797	33165	B	2830	1	614	
2798	33166	B	2831	277	528	
2799	33167	B	2832	1	1059	
2800	33168	C	2833	354	491	
2801	33169	C	2834	161	466	
2802	33170	B	2835	78	2700	
2803	33171	C	2836	37	111	
2804	33172	B	2837	1	1929	
2805	33173	B	2838	36	612	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
2806	33174	B	2839	189	498	
2807	33175	C	2840	302	430	
2808	33176	C	2841	58	219	
2809	33177	C	2842	56	275	
2810	33178	C	2843	21	293	
2811	33179	C	2844	337	543	
2812	33180	B	2845	1	507	
2813	33181	C	2846	232	489	
2814	33182	C	2847	314	476	
2815	33183	C	2848	572	937	
2816	33184	C	2849	259	528	
2817	33185	B	2850	1	597	
2818	33186	B	2851	1	564	
2819	33187	B	2852	368	732	
2820	33188	C	2853	58	375	
2821	33189	B	2854	608	1222	
2822	33190	C	2855	41	358	
2823	33191	C	2856	73	177	
2824	33192	B	2857	1	582	
2825	33193	C	2858	1	543	
2826	33194	B	2859	1	1538	
2827	33195	B	2860	40	704	
2828	33196	C	2861	303	407	
2829	33197	B	2862	131	336	
2830	33198	C	2863	64	156	
2831	33199	B	2864	180	712	
2832	33200	B	2865	1	1104	
2833	33201	B	2866	65	228	
2834	33202	B	2867	1	2172	
2835	33203	B	2868	1	1338	
2836	33204	C	2869	181	410	
2837	33205	B	2870	1	1137	
2838	33206	B	2871	69	1322	
2839	33207	C	2872	24	266	
2840	33208	B	2873	1033	1089	
2841	33209	B	2874	367	463	
2842	33210	B	2875	1	3256	
2843	33211	C	2876	278	466	
2844	33212	B	2877	323	4268	
2845	33213	B	2878	424	1711	
2846	33214	B	2879	567	643	
2847	33215	B	2880	1	258	
2848	33216	B	2881	1	806	
2849	33217	B	2882	56	984	
2850	33218	B	2883	1	807	
2851	33219	B	2884	1	396	
2852	33220	C	2885	107	411	
2853	33221	B	2886	1	678	
2854	33222	B	2887	1	246	
2855	33223	C	2888	41	316	
2856	33224	B	2889	1	300	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
2857	33225	C	2890	1	273	
2858	33226	B	2891	78	169	
2859	33227	B	2892	1	882	
2860	33228	C	2893	1	246	
2861	33229	B	2894	1	639	
2862	33230	B	2895	1	411	
2863	33231	C	2896	427	522	
2864	33232	B	2897	158	826	
2865	33233	B	2898	275	310	
2866	33234	B	2899	429	933	
2867	33235	B	2900	1	560	
2868	33236	B	2901	1	798	
2869	33237	B	2902	45	384	
2870	33238	B	2903	845	983	
2871	33239	C	2904	171	422	
2872	33240	C	2905	139	360	
2873	33241	C	2906	188	436	
2874	33242	C	2907	76	303	
2875	33243	C	2908	362	574	
2876	33244	C	2909	42	347	
2877	33245	B	2910	1	766	
2878	33246	B	2911	170	1381	
2879	33247	B	2912	274	543	
2880	33248	B	2913	768	2001	
2881	33249	B	2914	140	279	
2882	33250	B	2915	1	2858	
2883	33251	B	2916	1	321	
2884	33252	B	2917	1	552	
2885	33253	B	2918	1	603	
2886	33254	C	2919	122	406	
2887	33255	B	2920	508	679	
2888	33256	B	2921	1	942	
2889	33257	B	2922	1	753	
2890	33258	B	2923	136	326	
2891	33259	B	2924	445	625	
2892	33260	B	2925	1	639	
2893	33261	B	2926	1	1850	
2894	33262	B	2927	76	1341	
2895	33263	C	2928	184	495	
2896	33264	B	2929	1	226	
2897	33265	B	2930	1	972	
2898	33266	B	2931	57	1493	
2899	33267	C	2932	207	404	
2900	33268	B	2933	664	1647	
2901	33269	B	2934	1	1305	
2902	33270	B	2935	1	639	
2903	33271	B	2936	59	1108	
2904	33272	B	2937	276	1311	
2905	33273	B	2938	1	708	
2906	33274	B	2939	123	309	
2907	33275	B	2940	1	957	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
2908	33276	C	2941	199	357	
2909	33277	B	2942	319	355	
2910	33278	B	2943	574	1044	
2911	33279	B	2944	1	426	
2912	33280	C	2945	1	381	
2913	33281	C	2946	145	301	
2914	33282	B	2947	1	1644	
2915	33283	B	2948	1	906	
2916	33284	B	2949	249	317	
2917	33285	B	2950	388	655	
2918	33286	C	2951	228	379	
2919	33287	C	2952	200	343	
2920	33288	B	2953	1	600	
2921	33289	B	2954	123	719	
2922	33290	B	2955	1	879	
2923	33291	B	2956	88	445	
2924	33292	B	2957	518	1508	
2925	33293	C	2958	1	414	
2926	33294	C	2959	202	408	
2927	33295	B	2960	1	351	
2928	33296	B	2961	1	378	
2929	33297	C	2962	84	194	
2930	33298	B	2963	1	306	
2931	33299	B	2964	238	354	
2932	33300	C	2965	326	331	
2933	33301	B	2966	1	1005	
2934	33302	C	2967	31	408	
2935	33303	B	2968	48	335	
2936	33304	B	2969	1	241	
2937	33305	B	2970	1	768	
2938	33306	B	2971	93	728	
2939	33307	B	2972	25	88	
2940	33308	B	2973	1	414	
2941	33309	B	2974	1	555	
2942	33310	B	2976	83	3457	
2943	33311	B	2977	59	1280	
2944	33312	B	2978	1	414	
2945	33313	B	2979	1	354	
2946	33314	B	2980	1	477	
2947	33315	B	2981	1	357	
2948	33316	B	2982	182	394	
2949	33317	B	2983	148	1104	
2950	33318	B	2984	494	641	
2951	33319	C	2985	44	310	
2952	33320	C	2986	303	395	
2953	33321	C	2987	229	407	
2954	33322	B	2988	195	707	
2955	33323	B	2989	713	1063	
2956	33324	B	2990	67	746	
2957	33325	B	2991	468	1010	
2958	33326	C	2992	1	258	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
2959	33327	B	2993	1	282	
2960	33328	B	2994	139	767	
2961	33329	B	2995	1	133	
2962	33330	B	2996	136	291	
2963	33331	B	2997	172	634	
2964	33332	B	2998	1	435	
2965	33333	B	2999	503	1294	
2966	33334	B	3000	1	495	
2967	33335	B	3001	1	1416	
2968	33336	B	3002	1	321	
2969	33337	B	3003	1	378	
2970	33338	B	3004	1	337	
2971	33339	C	3005	1	474	
2972	33340	B	3006	1	633	
2973	33341	C	3007	142	423	
2974	33342	C	3008	226	360	
2975	33343	C	3009	45	281	
2976	33344	B	3010	1	369	
2977	33345	C	3011	2082	2558	
2978	33346	C	3012	99	356	
2979	33347	C	3013	312	467	
2980	33348	B	3014	89	463	
2981	33349	C	3015	16	357	
2982	33350	B	3016	239	541	
2983	33351	C	3017	176	345	
2984	33352	B	3018	1	2238	
2985	33353	C	3019	40	309	
2986	33354	B	3020	80	835	
2987	33355	B	3021	1	741	
2988	33356	B	3022	1	1005	
2989	33357	B	3023	185	3661	
2990	33358	B	3024	1	1539	
2991	33359	B	3025	1	1197	
2992	33360	C	3026	258	584	
2993	33361	B	3027	103	905	
2994	33362	B	3028	1	159	
2995	33363	B	3029	72	642	
2996	33364	C	3030	195	424	
2997	33365	C	3031	350	454	
2998	33366	B	3032	1	1494	
2999	33367	C	3033	1	336	
3000	33368	C	3034	169	423	
3001	33369	C	3035	131	307	
3002	33370	C	3036	80	423	
3003	33371	B	3037	1	663	
3004	33372	C	3039	619	1068	
3005	33373	B	3040	1	441	
3006	33374	B	3041	1	453	
3007	33375	C	3042	174	431	
3008	33376	B	3043	236	1145	
3009	33377	C	3044	99	215	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
3010	33378	B	3045	1	675	
3011	33379	B	3046	1	479	
3012	33380	C	3047	18	272	
3013	33381	C	3048	800	1097	
3014	33382	C	3049	1	231	
3015	33383	C	3050	1	777	
3016	33384	B	3051	194	328	
3017	33385	B	3052	1	633	
3018	33386	C	3053	431	838	
3019	33387	B	3054	1	450	
3020	33388	B	3055	684	1367	
3021	33389	B	3056	112	423	
3022	33390	B	3057	28	420	
3023	33391	B	3058	28	280	
3024	33392	B	3059	1	1335	
3025	33393	B	3060	516	1396	
3026	33394	B	3061	1	1563	
3027	33395	B	3062	1	903	
3028	33396	B	3063	191	628	
3029	33397	B	3064	1	534	
3030	33398	B	3065	1	1134	
3031	33399	B	3066	1	1248	
3032	33400	B	3067	1	1479	
3033	33401	B	3068	1	1635	
3034	33402	B	3069	46	447	
3035	33403	C	3070	1	624	
3036	33404	C	3071	25	330	
3037	33405	C	3072	132	253	
3038	33406	B	3073	4	1011	
3039	33407	B	3074	392	814	
3040	33408	C	3075	414	557	
3041	33409	C	3076	74	328	
3042	33410	C	3077	1	678	
3043	33411	B	3078	1	5130	
3044	33412	B	3079	1	985	
3045	33413	B	3080	1	1671	
3046	33414	B	3081	146	556	
3047	33415	B	3082	1	732	
3048	33416	B	3083	136	753	
3049	33417	B	3084	1	1500	
3050	33418	B	3085	300	2678	
3051	33419	B	3086	1	1221	
3052	33420	B	3087	58	1287	
3053	33421	B	3088	1	933	
3054	33422	B	3089	1	1317	
3055	33423	B	3090	1	771	
3056	33424	B	3091	1	2241	
3057	33425	B	3092	1	642	
3058	33426	B	3093	1	2664	
3059	33427	C	3094	1	513	
3060	33428	C	3095	52	174	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
3061	33429	C	3096	44	428	
3062	33430	C	3097	300	437	
3063	33431	C	3098	1	576	
3064	33432	B	3099	1	864	
3065	33433	C	3100	1	801	
3066	33434	C	3101	298	480	
3067	33435	B	3102	503	720	
3068	33436	C	3103	1	756	
3069	33437	B	3104	1	355	
3070	33438	C	3105	1	1143	
3071	33439	B	3106	1	2256	
3072	33440	C	3107	537	966	
3073	33441	B	3108	1	2009	
3074	33442	B	3109	1	3021	
3075	33443	B	3110	1	1085	
3076	33444	B	3111	180	2069	
3077	33445	B	3112	1	375	
3078	33446	B	3113	31	127	
3079	33447	B	3114	47	452	
3080	33448	C	3115	149	440	
3081	33449	B	3116	119	538	
3082	33450	B	3117	1	900	
3083	33451	C	3118	1	270	
3084	33452	B	3119	1	344	
3085	33453	C	3120	72	245	
3086	33454	B	3121	1	822	
3087	33455	C	3122	69	242	
3088	33456	B	3123	2129	2289	
3089	33457	C	3124	1	255	
3090	33458	B	3125	2129	2289	
3091	33459	B	3126	1	306	
3092	33460	C	3127	1	255	
3093	33461	B	3128	82	1254	
3094	33462	B	3129	1	468	
3095	33463	C	3130	2	250	
3096	33464	C	3131	166	357	
3097	33465	B	3132	423	3286	
3098	33466	B	3133	63	436	
3099	33467	B	3134	1	4578	
3100	33468	B	3135	1	4322	
3101	33469	B	3136	46	325	
3102	33470	B	3137	58	289	
3103	33471	B	3138	1	1695	
3104	33472	B	3139	89	1195	
3105	33473	C	3140	317	541	
3106	33474	B	3141	314	992	
3107	33475	C	3142	95	222	
3108	33476	C	3143	26	172	
3109	33477	C	3144	40	255	
3110	33478	C	3145	277	508	
3111	33479	B	3146	12	1358	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
3112	33480	B	3147	602	780	
3113	33481	C	3148	1	306	
3114	33482	C	3149	1	771	
3115	33483	B	3150	149	360	
3116	33484	B	3151	1	567	
3117	33485	B	3152	1	345	
3118	33486	B	3153	1	1233	
3119	33487	B	3154	144	773	
3120	33488	C	3155	1	417	
3121	33489	B	3156	85	525	
3122	33490	C	3157	251	679	
3123	33491	B	3158	1	1185	
3124	33492	C	3159	541	729	
3125	33493	B	3160	211	382	
3126	33494	C	3161	200	409	
3127	33495	C	3162	85	423	
3128	33496	C	3163	243	455	
3129	33497	B	3164	152	437	
3130	33498	B	3165	1	816	
3131	33499	B	3166	79	294	
3132	33500	C	3167	6	353	
3133	33501	C	3168	82	405	
3134	33502	B	3169	3	191	
3135	33503	C	3170	204	413	
3136	33504	B	3171	75	1449	
3137	33505	B	3172	1	738	
3138	33506	B	3173	1	324	
3139	33507	C	3174	299	1009	
3140	33508	B	3175	1	447	
3141	33509	C	3176	1	570	
3142	33510	B	3177	1	703	
3143	33511	B	3178	142	744	
3144	33512	B	3179	1	237	
3145	33513	C	3180	63	254	
3146	33514	B	3181	185	330	
3147	33515	B	3184	214	1333	
3148	33516	B	3185	61	423	
3149	33517	B	3186	19	2467	
3150	33518	B	3187	4	1085	
3151	33519	B	3188	157	341	
3152	33520	B	3189	222	656	
3153	33521	B	3190	249	999	
3154	33522	B	3191	416	2447-	
3155	33523	B	3192	187	1855	
3156	33524	C	3193	38	166	
3157	33525	B	3194	1	1449	
3158	33526	B	3195	286	663	
3159	33527	B	3196	255	556	
3160	33528	B	3197	85	591	
3161	33529	B	3198	32	404	
3162	33530	B	3199	185	253	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
3163	33531	B	3200	202	2862	
3164	33532	B	3201	448	833	
3165	33533	B	3202	1	1275	
3166	33534	B	3203	1	591	
3167	33535	C	3204	1	291	
3168	33536	B	3205	1	744	
3169	33537	B	3206	338	523	
3170	33538	B	3207	1	435	
3171	33539	B	3208	1	477	
3172	33540	B	3209	1	2943	
3173	33541	B	3210	1	1719	
3174	33542	C	3211	113	280	
3175	33543	B	3212	1	1092	
3176	33544	B	3213	1	1470	
3177	33545	B	3214	1	426	
3178	33546	B	3215	1	747	
3179	33547	B	3216	321	2234	
3180	33548	B	3217	1	3057	
3181	33549	B	3218	1	537	
3182	33550	B	3219	1	2496	
3183	33551	B	3220	94	273	
3184	33552	B	3221	302	1432	
3185	33553	B	3222	35	1657	
3186	33554	B	3223	2	901	
3187	33555	B	3224	82	1479	
3188	33556	B	3225	224	411	
3189	33557	B	3226	328	429	
3190	33558	B	3227	27	1098	
3191	33559	B	3228	508	1765	
3192	33560	C	3229	1	321	
3193	33561	B	3230	251	415	
3194	33562	B	3231	695	1011	
3195	33563	B	3232	1	416	
3196	33564	B	3233	45	1340	
3197	33565	B	3234	65	2087	
3198	33566	B	3235	1	1149	
3199	33567	C	3236	1	108	
3200	33568	B	3237	1	384	
3201	33569	B	3238	80	383	
3202	33570	B	3239	200	409	
3203	33571	B	3240	14	419	
3204	33572	B	3241	1	888	
3205	33573	C	3242	165	435	
3206	33574	B	3243	452	593	
3207	33575	B	3244	1472	4415	
3208	33576	B	3245	103	207	
3209	33577	B	3246	242	292	
3210	33578	B	3247	1	306	
3211	33579	B	3248	1	684	
3212	33580	B	3249	1	838	
3213	33581	B	3250	215	2593	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
3214	33582	C	3251	80	376	
3215	33583	B	3252	1	639	
3216	33584	C	3253	52	288	
3217	33585	B	3254	1	1197	
3218	33586	B	3255	39	2809	
3219	33587	B	3256	1	609	
3220	33588	C	3257	269	418	
3221	33589	B	3258	1	561	
3222	33590	B	3259	347	922	
3223	33591	B	3260	52	339	
3224	33592	B	3261	235	434	
3225	33593	B	3262	74	2676	
3226	33594	B	3263	90	675	
3227	33595	B	3264	1	1440	
3228	33596	B	3265	288	752	
3229	33597	B	3266	1	804	
3230	33598	C	3267	109	451	
3231	33599	B	3268	1	1122	
3232	33600	B	3269	1	768	
3233	33601	B	3270	380	2743	
3234	33602	B	3271	1	1296	
3235	33603	B	3272	322	591	
3236	33604	B	3273	174	464	
3237	33605	B	3274	1	384	
3238	33606	C	3275	320	385	
3239	33607	B	3276	53	485	
3240	33608	C	3277	175	205	
3241	33609	B	3278	216	316	
3242	33610	B	3279	1	921	
3243	33611	B	3280	22	453	
3244	33612	B	3281	168	817	
3245	33613	B	3282	1	477	
3246	33614	B	3283	190	1062	
3247	33615	B	3284	116	787	
3248	33616	B	3285	130	697	
3249	33617	B	3286	1	901	
3250	33618	B	3287	1	342	
3251	33619	B	3288	1	677	
3252	33620	B	3289	1	624	
3253	33621	B	3290	1	756	
3254	33622	B	3291	1	624	
3255	33623	B	3292	130	429	
3256	33624	B	3293	95	516	
3257	33625	B	3294	120	524	
3258	33626	B	3295	51	425	
3259	33627	B	3296	647	1015	
3260	33628	C	3297	518	841	
3261	33629	C	3298	67	294	
3262	33630	B	3299	1	1212	
3263	33631	C	3300	187	453	
3264	33632	B	3301	188	492	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
3265	33633	B	3302	123	647	
3266	33634	C	3303	1	219	
3267	33635	B	3304	1	690	
3268	33636	B	3305	1	930	
3269	33637	B	3306	552	722	
3270	33638	B	3307	84	304	
3271	33639	B	3308	328	1104	
3272	33640	C	3309	300	593	
3273	33641	C	3310	1	87	
3274	33642	B	3311	1	819	
3275	33643	C	3312	122	334	
3276	33644	B	3313	1	318	
3277	33645	B	3314	764	977	
3278	33646	C	3315	379	471	
3279	33647	B	3316	1	1194	
3280	33648	B	3317	1	1800	
3281	33649	C	3318	273	506	
3282	33650	B	3319	1	1689	
3283	33651	C	3320	48	212	
3284	33652	C	3321	1	507	
3285	33653	C	3322	117	251	
3286	33654	B	3323	89	845	
3287	33655	C	3324	1	651	
3288	33656	C	3325	48	212	
3289	33657	C	3326	1	864	
3290	33658	B	3327	223	839	
3291	33659	C	3328	1	189	
3292	33660	B	3329	36	144	
3293	33661	B	3330	56	389	
3294	33662	B	3331	1	597	
3295	33663	B	3332	1	606	
3296	33664	C	3333	1	426	
3297	33665	B	3334	1	696	
3298	33666	B	3335	1	417	
3299	33667	C	3336	1	594	
3300	33668	B	3337	1	228	
3301	33669	C	3338	1	879	
3302	33670	B	3339	1	405	
3303	33671	C	3340	33	152	
3304	33672	B	3341	224	429	
3305	33673	B	3342	578	4588	
3306	33674	B	3343	1	288	
3307	33675	B	3344	77	1479	
3308	33676	B	3345	132	875	
3309	33677	C	3346	120	395	
3310	33678	B	3347	1	729	
3311	33679	C	3348	8	133	
3312	33680	C	3349	171	359	
3313	33681	B	3350	1	1098	
3314	33682	B	3351	1	1547	
3315	33683	B	3352	1	933	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
3316	33684	B	3353	1	1989	
3317	33685	B	3354	1	595	
3318	33686	C	3355	62	559	
3319	33687	B	3356	1	153	
3320	33688	B	3357	1	768	
3321	33689	B	3358	1	969	
3322	33690	B	3359	217	358	
3323	33691	C	3360	449	961	
3324	33692	B	3361	1	1799	
3325	33693	B	3362	80	1327	
3326	33694	B	3363	111	258	
3327	33695	B	3364	112	429	
3328	33696	B	3365	147	390	
3329	33697	B	3366	1	585	
3330	33698	B	3367	1	2290	
3331	33699	B	3368	19	4071	
3332	33700	C	3369	1	183	
3333	33701	C	3370	1	183	
3334	33702	C	3371	44	283	
3335	33703	B	3372	1	954	
3336	33704	B	3373	1	384	
3337	33705	B	3374	709	773	
3338	33706	B	3375	1	3294	
3339	33707	B	3376	83	1229	
3340	33708	B	3377	1	1512	
3341	33709	C	3378	30	200	
3342	33710	A	3379	3	322	
3343	33711	A	3380	530	1489	YAGNESHPPSLPRYLRRSRHCG CRPPPLPVPTPTQACNAPQRRR TTSTSLACLGRAGLWLPSVSSP YLVLSSCQEQPHHCCPPSTPRPS WSPLPGMPSA/SSPGQVPAQGD LSQEDSSDSPPAEQVLPPSSGSH NTLYLGCKRFSAFILNCEPPSKL LKARPQVSELSWNPDFVAS/SA ARPRDGPCSTGRQSASKTPPPPS HPHTGHSLWSEEK*KDSDSRPN QSAFPGCSVDLQFSHKLRPYLI HP/SESLGTVGNRPSQEGHELPP APFSRMGPEQHLPVVVLPFTGA FAVVLPCPFLVSSSAWHFKVKH PSIPLLRGEK

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3344	33712	A	3381	296	1255	YAGNESHPPSLPRYLRRSRHCG CRPPPLPVPTPTQACNAPQRRR TTSTSLACLGRAGLWLPSVSSP YLVLSSCQEQPHHCCPPSTPRPS WSPLPGMPSA/SSPGQVPAQGD LSQEDSSDSPPAEQVLPPSSGSH NTLYLRCKRFSAFILNCEPPSKL LKARPQVSELSWNPDFVAS/SA ARPRDGPCSTGRQSASKTPPPPS HPHTGHSLWSEEK*KDSDSRPN QSAFPGCSVDLQFSHKLRPYLI HP/SESLGTVGNRPSQEGHELPP APFSRMGPEQHLPVVVLPFTGA FAVVLPCPFLVSSSAWHFKVKH PSIPLLRGEK
3345	33713	A	3382	81	702	RAAFSPPAPVSSLPAPVSSPPAS TSCPPAPVSSLPAHASSPPASTSS PPAPLSSAPAHTSSLPAPVSSPP ASTSSPLVAGSGGSTTRSLPPGL GALLTHSVAPYPGGQPPPAAAD DP*TMAPAGWGSHNPRGCSCSP VAAGAGPFPASF*GPLR*AGSQ TFQILQVEVFLVVRHFSPSTP/PS VMLYPPPPSTPPTLRAPRPPIPPS P
3346	33714	A	3383	3	231	PMLLEVSVADRDAV*TFWQAPI GESQQGALGFWSKALQSSADN NS/PFQITMQPELPIMNWVLSVP SSHKMGHAQQH
3347	33715	A	3384	3	355	KIPGTSTSVKFLGVQ*CGTCQDI PSKVKDKLLHLAPPTIKKEAQR LVGLFGFWSQHIPHLGELLRPIY RVTRKAASFEWGPEHEKALQQ VQAALQAALPLGPYDPADQPL CNLNCLS

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3348	33716	A	3385	2	1076	LCQRLLLAEPNEKPGSLGNVM AVARIEIGICEYYHEKTTEKALD SHGVLAGSTIKGVRSFQRNLEL KLPATERATANAIELLTVLDQA YENFAPQILPSTGSPTSQETAQF KANQNKPLVRGKGSPHEAIRYI SAAHREWKPAILTSAIRSFCST WLVFTSKNFPKLVTQHGSTIAG NGQSSDETQVQGAAWKSDSRG TKRQIPTWILAEGNNAGAQLDI PGPTIPAPNCSLKVPQSWSTTPS MPSSLGKAYWLLACYWALVET E/RLAMGHQVTM\KPELPVMN WVLSDPSSHKVGGAQQHSINK WKWYIRNRARAGPEGTTLPLT KALTLWLKKYSNVLMLVEFTG LTMFPDILKQLE
3349	33717	A	3386	1	1416	MAQYPILDFLKVGQLLGNCAL GKGNDQTFRGLLDTGSELTLIP GDPKHHCDPPVKCAAIDLANA FFSIPVHKAHQKQFAFGWQGQ QYTFTVLHQGCMNSLALCHNLI QRELDCFLTPEDITLDHYIDDIM LIGSSEKEVANTLDLLFWDYRH EPLRLANYSPFERQLLACYWAL VETECLMMGHQVTMRPELPIM NWVLADPSRHKVGNAQQHWK CAVHT/IIKWKWYIRDWAQAG LEGTS*LYWPRASRYQQGHQD LFILRSDLPSQVFIRDKLMERRN RRTGRTEKARIWEVTDRTVRT WIGEAVAAAAADGVTFSVPVT PHTFRHSYAMHMLYAGIPLKV LQSLMGHKSISSTEVYTKVFAL DVAARHRVQFAMPESDAVAM
3350	33718	B	3387	50	693	
3351	33719	A	3388	153	578	ARIQ/GSRNQGVEVEVAPLTVT PSDPLANVLLPVPATLPSAGLEI LVPEEGRLPPGDTTMMPLNWN LRLPHGHFGLLLPLNQQAKKG VAVLGGVIALDCQDEISLLLYK GDLTVMVEDKEEQNHILHGSR QREREPSKTGSPL
3352	33720	A	3389	3	402	GRHAVGDIEAEDGGGVRGPHP GGVYGLQQSHPGGGDPVWED GHPGLPGAQQRGQ*RQQACAH HKSPSGAG*G*LPGP/AQS/AGN PDPKSPGPAPCLVGSSRNETPG AMGAPSRNGSPPTAGLGVGDG TGSPSEAV
3353	33721	A	3390	141	320	

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3354	33722	A	3391	1	464	HLKGLGNDTPRVCSCLIG*T*LC DCH*LQ\EASPTSVEVREPRTSV NKD/SPKSLLYSCSYSYFDEPVE LRSSSFSSWDDSSDSYYETHLL HLKLV*PNLAVFNCRPTARRKP DYEPVENTDEAQKTFCKTAHN LWSLTFPFPCLL*YETRARLER
3355	33723	A	3392	3	1189	
3356	33724	A	3393	1	867	PGRPT/LSEWI/QNTLGVNVEHK TTSKASLNPRDTPPSVVNEDFL HDLKETNISYSQEADDRVFRAH GHCLHEIFLLTEGMFERIPDIVL WPTCHDDVVKIVNLACKYNLC IIPIGGGTSVSYGLMCPADETRT IISLDTSQMNRILWVDENNLTA HV*AGITGKELERQLKESG\YCT G\HEPRFPWSSSTVGGWVSTRA SGMKKNIYGNIEDLEIVHFSDN DLSCIELDRLIEIVLPSSGIPLLD GYSTEIHMPVHLETSTTMCIVTP IHSSMKLETLRMSMSINCRKDK
3357	33725	A	3394	1	890	MSKSESPKEPEQLRKLFIGGLSF ETTDESLRSHFEQWGTLTDCVV MRDPNTKRSRGFGFVTYATVE EVDAAMNARPHKVDGRVVEP KRAVSREDSQRPDYFEQYGKIE VIEIMTDRGSGKKRGFAFVTFD DHDSVDKTVIQKYHTVNGHNC EVRKALSKQEMASASSSQRGRS GSGNFGGGRGGGFGGNDNFGR GGNFSGRGGFGGSHGGGGYGG SGDGYNGFGNDGSNFGGGGSY NDFGNYNNQSSNFGPMKGGNF GGRSSGPYGGGGQYFAKPRNQ/ GGYGGSSSSSSYGSGRRF
3358	33726	A	3395	2	441	DGMEKVDTAMNARPHKVDGR FVEPKTAVSREDSQRPGAHLTV IKM/FKE/DTEEHKLRDYIEQYG\ GGNFSGCAGFGGRSGGGR*GG SGNGYNRFDNDGSNFGGGGSY NDFGNYNDRSSNFGPIKGGNFG GRSSGPYGGGSQYFAKP*NQ
3359	33727	A	3396	3	404	

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3360	33728	A	3397	2	762	MNARPHKVDGRVVEPKRAVSR EDSQRPGAHLTVKKIFVGGIKE DTEEHHLRDYFEQYGKIEVIEI MT\DRGSGRKRGFVFVTF\DDP\ DSVDKIVIQKYHTVNGHNCEV RKALSKQEEMASASS\SQRGRS GSG\NFGGGRGGGF\GGNDNFG RGGNFSGRGGFGGSRGGGGYG GSGDGYNGFGNDGSNFGGGGS YNDFGNYNNQSSNFGPMKGGN F\GGRSSGPYG\GGGQYF\AKPR\ NQGGYGGSSSSSSY\GSGRRF
3361	33729	A	3398	1	3737	
3362	33730	A	3399	5	633	DLREWSWARRTAWEPRGKRV RGK*AFKEIQCP*QQKE/SMSGL LLLKVVAKEMTWLPPLSAIQAP GKVEPTKFPFPNKLMFSWWYIE TTTASAKVIGYKPSVLNCATLR VQIMSHYHSYRHLASLLVEGSA TLPGHSHILGPLIRHPDKVSAGK PRVLGLQLLKEDCSSQPAAKPQ GPHRLCSSLILHRARARLGPEQ RETKVPFSKGTTH
3363	33731	A	3400	2	816	QVPTMVDWAGWSPGLWTTCS GTGGGGAEQGWANWSLVLPG VLAGTSLETFSPLS*GLTFSSLLL MQISAASLNFSSENGIFFSTTLP GCKFSKFLCSASLLKWNAFSST QVTS*MLCCSEISSTRYPKSSL* SSKFHKSLEQGQNAASLFAKT* QESPLLQLPTSSSSPSETTSAWIS LSISLSVFLSKLFDKSLESSKLS\ TFSSVLLSPPNCSNLCLLPSFKV ACTFLGTFLRSTSLHWYQFTVL VCFHPADKDILKSEKKKRCKEK
3364	33732	A	3401	1	485	LFKAVLHDPHLKLLSLYGTSLS HTDVSHLCETLKHTTCKIEELM LGTCDISDEGCEDIASVLACNS KLIHLSLVENPEKDKRM\CCCA LETLMLMYCCLICVSCEDISHV LFCSKSLSLLDLGSNFLEDNEV\ HLLCEALKH*DACKTWRSLNF DWVGYLGC
3365	33733	C	3402	952	1164	

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3366	33734	A	3403	3	163	IAVSKQDPITSLEQEKEPWNMK ICEMVDESPAMCSSFTRDLWPE QDIKDSFQQVILRRHGKCEHEN LQLRKGSASVDEYKVHKEGYN ELNQCLTTTQSKIFPCDKYVKV FHKFLNANRHKTRHTGKKPFK CKKCGKSFCMLLHLSQHKRIHI RENSYQCEECGKAFKWFSTLTR HKRIHTGEKPFKCEECGKAFKQ SSTLTTHKIIHTGEKPYRCEECG KAFNRSSHLTTHKIIHTGEKPYK CEECGKAFNQSSTLSTHKFIHA GEKPYKCEECDKAFNRFSYLTK HKIIHAGEKP\YNCEECGKGFN WSSTLTKHKRIHTGEKPYKCEV CGKAFNESSNLTTHKMIHTGEK PYKCEECGKAFNRSPQLTAHKII HTGEKPYKCEECGKAFSQSSIL TTHKRIHTGEKPYKCEECGKAF NRSSNLTKHKIIHTGEKSYKCEE CGKAFNQSSTLTKHRKIHTRQK PYNCEECDNTFNQSSNL/N*/HK IIHTGEKLYKCQECGKASKQSF TLTKH*ILFNK
3367	33735	A	3404	3	345	
3368	33736	B	3405	282	694	
3369	33737	A	3406	586	1403	VSETALADGRCWFRKCQSHLC LASTTGKC*TSTLQSGRDYTEN GESAQEGETGLPERRLAHCT*L AEVHRRQPD*TQENRP/SKMGI MTSS/AAKDHLDNKCQRQDSIP GSSRGPSPLTMGAQDTLPVAAA FTETVNAYFKGADPSNTPSVLV EQLLSKRRSNPIMDHGGHKVPC SLPPLLTHPNRRQRELKMYGSH KAVAQPSPLQDRLQQCAVPTP VTGWTNSRAALGDIFSTWGSLL LRTSTPKKAAARARPMCPCPGA YNTSYPLAPYFWR
3370	33738	A	3407	1	421	FRHSMNGCEKDSSSTDSANEKP ALIPREKKISILEEPSKALRGVT GPNIEKSVKDLQRCTVSLTRYR VMIKEEVDSSVKKIKAAFAELH TCIIDKEVSLMAEMDKVKEEA MEILTARQ\RKAEALKRLTDL\A S\QMAEMQL
3371	33739	A	3408	1	403	MEILTARQKKAEELKRLTDLAS QMAEMQLAELRAEIK/*WFSEN ELGNSDLCSYSCYCLAAQKLSC QCYLGGTAHSAPGIAKRKTSQL I*PLP

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3372	33740	A	3409	1	756	
3373	33741	A	3410	2	1849	QRRRRNTPGWSGFQGLTRAPA LFPRLIFQSSSETRLLSGTLLWIP RAYSTRSKMAELNTHVNVKEK IYAVRSVVPNKSNNEIVLVLQQ FDFNVDKAVQAFVDGSAIQVL KEWNMTGKKKNNKRKRSKSK QHQGNKDAKDKVERPEAGPLQ PQPPQIQNGPMNGCEKDSSSTD SANEKPALIPREKKISILEEPSKA LRGVTEGNRLLQQKLSLDGNP KPIHGTTERSDGLQWSAEQPCN PSKPKAKTSPVKSNTPAAHLEI KPDELAKKRGPNIEKSVKDLQR CTVSLTRYRVMIKEEVDSSVKK IKAAFAELHNCIIDKEVSLMAE MDKVKEEAMEILTARQKKAEE LKRLTNLASQMAEMQ\LAELR\ AEIKHFVSERKYDEELGK\AAR FSCDIEQLKAQIMLCGEITHPK\ NNYSSRTPLQAPCWPLLNA\HA ANLWGKQSNF\SRKSSTHNKPS EGKAATPKMVSSLPSTADPSLR AMPANKQNGSSNQRRRFNPQY HNNR\LNGPAKSQGSGNEAEPL GKGNSRHEHRRQPHNGFRPKN KGGAKNQEASLGMKTPEAPAH SEKPRRRQHAADTSEARPFRGS VGRVSQCNLCPTRIEVSTDAAV LSVPAVTLVA
3374	33742	A	3411	1	489	MAEVQVPVLHGRGHLLGRLAA IVAKQVMLGWKVVVVRCEGIN ISGNFYRNKLNCSFRTPSCIFRW TVRGMLPHKTKRGQAVLDHLQ VFDGISPLYDK/K/KRMVVPAAL KVVRLKPTRKFAYLGRLAHEV GWKYQAVTATLEKRKEKA*IH YRKKKQLMRLRKQA
3375	33743	A	3412	2	260	
3376	33744	A	3413	1	612	AEVQVLVLDGRGHFLCRLADI VAKQVLLG\RKVVVVRCEGINI SGNFYRNKLKYLAFLRKRMNT NPSRGP\YHFRAPSRIFWRTVRG MLPHKTKRGQAALDRLKVFDG IPPPYDKKKRMVVPAALKVVR LKPTRKFAYLGRLAHEVGWKY QAVTATLEEKRKEKAKIHYRK KKQLMRLRKQAEKNVEKKIDK YTEVLKTHGLLV

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
3377	33745	A	3414	734	1488	MTKDPWLKQSGSSDTSPAASP GHFRAVPRAPRARGTVVHHRH/ LCLSSWPSSS/RVPPGCASYTPA STAAGALPYQAQRRQGVLRRY TTYLRV*HFLPRGLPEGFQRGP RVPPPPPCPMAAEPELGHALKL LD\LREIVSFLYYFFFFFLRRSLT LSPGWRDLGSLQ\PLPHGFKAIF /SCFSLLSGWD\YRHTATHAQLI FVFLVEMGF/TPMFARMASIS*P CDPPDSASQDAGITGVSHQVW RERLFLDEGGGGCP
3378	33746	A	3415	48	966	WSQVVTIVTVVVTVSGSNHGN HTQASHEGYRHPMRAQVSH/G ECR/PSHEGHRHPMRTQASHEG HRRPMRTQASHEGHRHPMRTQ ASHEGHRHPMRGTGVP*EHRH PMRAQASH/GEHRR/HH/GEHSC PMRAQASHEGTGVP*EHRC/HH ENTGVP*GHRCPMRMQASHAG HRHPMRVQASHEGHRCPMRTQ VSHEGHRRPMRVQASHENTGV P*GAQASHEGTGVP*EHSHPMR AQASHENTDVP*GVQASHEGY RRPMRTQASHEGHRCPMRAQT SHENTGVP*AAQYRP*EAGAPQ GGQGWQETGADRST
3379	33747	A	3416	8	432	NSKLPPVVTSQQMRFMY/DPQT DQHMKI\FPEQLPLDEFLQKTDP KDPANYILHAVLVHSGDNHGG HYVVYLNPKGDGKWCKFDDD VVSRCTKEEAIEHNYGGHDDD LSVRHCTNAYMLVYIRESKLSE VLQAVTDHDIPQQL
3380	33748	A	3417	38	2865	SFRWDSKKHTGYVGLKNQGAT CYMNSLLQTLFFTNQLRKKLL MGALPWEGALAPWV*ALDTDP SLPCSTCLTTARTCTSL\QQCHA DQCRWQTRWQGSSRW*WQQE EIGQEREEGVEYAKRVLLGPPY SISDCTHMESSLPPCSS*DPGSF QFHEERAEDEKSEGRGPSCSCT QPPPW*SLGEGLGECR*ESSSSY CSLAGLSLHP*ETRGERLQEAS QGQPESPFGEV*HPALVSLDLA E*QGRAEKHGCTETH

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3381	33749	A	3418	2	3515	YVRVSLPPPPPAAGRPGAAVAD DAREEEEEAAPPPPPPPPPRLAA ARPPGSQPRPPAAGEAQAAAD MNHQQQQQQQKAGEQQLSEPE DMEMEAGDTDDPPRITQNPVIN GNVALSDGHNTAEEDMEDDTS WRSEATFQFTVERFSRLSESVLS PPCFVRNLPWKIMVMPRFYPDR PHQKSVGFFLQCNAESDSTSWS CHAQAVLKIINYRDDEKSFSRRI SHLFFHKENDWGFSNFMAWSE VTDPEKGFIDDDKV
3382	33750	B	3419	36	335	
3383	33751	A	3420	2	1602	CRLKTTAFSSPSSRHITACLPRF WQICSLPKHLIPPEAPPVGMS*R RRKPVWVKSMMLG*RIP*GKR DPPTTAKCRTCSPQEETGPAGT QGQAARQLERRKLPPYVQT/PP RPDQLKGVCSLQTDAISLAPTA ERHSRLLPPPSRQQPTSAGTEA GACPNTRRPSGLQLPAAV\QTPS GQTPSVPKPGLEPTSLPVGSG/PI SASHSQ/PVSKINKK**VCESPY METFP*DAKRTRHKRADTARR GEPLRPRTSVPRRTVPAPSEKLR GSRRGEPTPAAPRRDPRRAGSL THAGPPGG*RHR*PGWPRGTA/ AKTPVAAEALIAAAAPLALHRI PLGAPPQLPAAPAP/RLALALRG ASAA/RPRVAPSAASPQRCLLR\ GPPSPQPSPAPGPVAPSAQGRG AVPGGVLAVLLPGAPRLSGKRP AAPRGGDTPAQGQVPLAARAP REGPGHGREPVIEELERRGAEL RSGKGGTRSEGVRGGRARGIV YGGAHGPEVGKDKMPLKPRNL SAPVAIGGLLHGAGIRFLNLAL HSPAVDFGQIT
3384	33752	A	3421	3	498	IIDPTQYRPMVPNKVSSPC*WLP TITQVHPDNEAEPIPS/PARSCAP ICGVP/AYGSPLSQSSVS*TRQ*F PSCSQSL**GSPTLVNPKTAYT* NSGSRGG/VSFDEDTSQHCYPG TG*GQQPLQ*SRNHAGPPGG*M T*VTGVAERDK/PPKTPVGRRG THSQPPRRSP
3385	33753	A	3422	1	270	

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3386	33754	A	3423	1	1899	MGFCHIGQAGLKLLTSKDLPAS AFQSAGIAGFWLLDGISGPILGQ REACCPAGNSNKELKQENSAL AEQLQVVLIDKAGMQCDLEEL KKKLELTELTLQQLSSWCEAPD ANQQLQQPTDERAQLEAHLGQ VMEWLKYLQMEREQYAEYLH GESAMWWQRMREMSEQIGHLI VPGICEMGGAQPEVVMGLGFV EVHTLREERVHSMSRVQELETI LAELRNQVAEPLPPEPPAGPSE VEQKLQAEAEHLWKELENLAG QLQAQVEENEGLSHLNQEQE\G LLRLLEQEEKLLEQEERLLEQE ERLLEQEERLLELQESLLEQKR KAASFLS*TPTPGAPSRALRGK YVTSYQSQRSV/REDVDRENEY ISRLAQDKEEMKVKLLELVLQL VGDCNKWHGRFLAAAQNPAD EPAPWDPAPQEIGAANKQGGLF PGCCLVTPGGFHGDCRGAYGA QSSPDSQQAQNPDLAVAGKAA FWEFKEHQESLTLLKSWGRRK SGSGQAAQLREGSRCAAARRH LARALPAARMPKRKVISTEGAA KEEPKRTSASLSAKPPAKVEAQ PKKAAAKDKSSDKKTQTKGKR GAKGKQAEVANQETKEDLPAE NELSSLYSFYARSLILAFIIHLRM
3387	33755	A	3424	198	364	FLII*YEGINCSRIVNLTRTAWCF FSG*IFRQKKCKQKGKGEQREN RPEVANPRN
3388	33756	A	3425	3	238	GVCPPRGRSCSDFKADSLYSFP CPSRCGS*ESSTQTCSGFWTGCT ALHRWRGMPERCPPESRDS*TR FPQSSLPGHKT
3389	33757	A	3426	3	681	HIRGPRYSGHHSAFGCPYSDMN LKKEATLHDRLREQTQAN\LES DSSHSKSKSLCSLNFNGKHEKV NSQPRLVQQAKCLKIKGKEDID LDNLFREYSVEQAQQVLHQSV SMSTVSAHPFRDLPLGREQHCK LLPGVADIRASQVARWTVDEV AEFVQSLLGCEEHAKCFKKEQI DGKAFLLLTQTDIVKVMKIKLG PALKIYNSILMFRHSQELPEEDI ASGQEVRG

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3390	33758	A	3427	30	981	TQDPWPSLPVLWSRASSDPAAG HRAEHI*TYWPWKLEGT\DIWL VLYMPLVQPDNFIKKHSHLPTY CLFKEDVKFPFRTCRLTYCWLN YTEEITYLHTKKVSVGQSAVRE EFAAACTWSIRIGEKLAILLSLY LCRQQALLNMRMSVPIHESGV AQRSPVMDKLAQYSVEQAQQV LHQSVSMSTVSAHPFRDLPLGR EQHCKLLPGVADIRARQVARW TVDENLHGLIQTKQTPHLDESIS KGESPALVVTELRMCMTATEP LVPTKNPYQERGHIGDSFLHYT DQEPQPWDQSSVHPTPAPIYSV SSGFRVTRGSDI
3391	33759	A	3428	1	864	MVSALPEVGRAQILRLIAYIRSP APPVVGVERAARRPAQAFGLV ALPSTDATVFANQPLARACIGA ARHREPDAPGQSAWVGEECLK DALRSPETPKLGSLSPPCQDTRP GRASNDFSLEMGYSSLSAARLK IHGQVFQCCGPGPLRTL\HWTQ S*TYLNILALET*GAQNQP*EW QAVD*GAPGLFSHTLGVFPR/RL PQHPKQIICFQNYEYSVEQAQQ VLHQSVSMSTVSAHPFRDLPLG REQHCKLLPGVADIRASQVAR WTVDEPYSSAPRGPELSAGANS SRGA
3392	33760	A	3429	201	336	QQTPGKAVHAPFIADQSLT*EL VSVFPQFQLFPYRR*DSHSGKS
3393	33761	A	3430	600	768	TDTSSYHGSG*PAR/NG*MHSFI RCLLLK*GIEPCALNGDSVLKS RTDVTFTPVNITTKVKSVEMHN EALSRALPGDNVGFKNVSKMF VMATLLFSDCIHNTFDQMWRT KEHNEARWSLQSSGDKVMKEN DELRDSVSQLQKQTLSLKSPKI ALGESLISCRERAEIEIVDKQTQ ALIMGVADLQGRVNAQLHQVS TVKVRDWKRMGPYNLECGTV GRTLIKLWTLSL
3394	33762	A	3431	1655	1841	EHQAEAEGGDGGPRSLPMKPG SPLMPDKAQRKQVRSRHGRGG RGGG*AGPGIPGKPGSPVSP
3395	33763	A	3432	1	1773	

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3396	33764	A	3433	648	1884	LDPEVAWAKWQHSTVKGPQK QFAFSWQGQQYTFTGLPQGYIN SLSLCYNLIPRDPD/RL/SLLQNI TLVHYIDDIMLIGSSEQELAYTL DLLVRRLCAKGWEINLTEIQEA STSVKFLRVQWCGACQDIPSK MKDKLLHLFPPTTKKKASLFGF RRQCIPHLECGPEQEKALQQAQ AAVQAAVPLERYDPADPMVL/ V/ELTWLWPLLSAQFASSGDQH *ALHMAPFLGVVSQLPGGKLIIL DIFHHGKGRVLFSLE*TLTPDM GLPILHIMLLPRLPSVNSQNALS TVMPGFTGPGIKGWKWHHSPS PLVIH*QNFCFLFP*HYVLLA*R S*FQRKEPCHQET*Q*FH*TGS* GCQLDTLGSCYF*VNKLRRELQ CWLG*LTQTIKMKSVYYSITEN CWMKRSPVKRRKILELEEA
3397	33765	A	3434	1	2223	
3398	33766	A	3435	1	1078	MNKEMSGQTFVGKQNSVRMP KIISGLGVQKPNRQWRLVQDLR IINEAVVPLYQAVRNPYTLLSQI PEETGWFTVLDLKDALFCIAVH PDSQFLLAFEDPLNPTSQLTWT VLPQGFRDSPHLFGQALAQDLS QFSYLDTLVLRYVDDLLLAAPS ETLCHQATQVLLNFLATCGYK VSKLKAQICSQQVKYLGLKLSK GTRALSEERIQPILAYPHPKTRK QLRGLLGITGFCQIWIPRYSEIA RPLHTLIKKTQKANTHLVRWTP EAEAAFQVLKKALTQAPVLSLP TGQDF\SLYVTEKTGIALGVLTQ HYGEERNS*LPTEYLSNIRKPLG DYYWLYRNLKRWQSYTARVIR KERKGK
3399	33767	A	3436	1	1677	

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3400	33768	A	3437	1	2052	MVLVVVAVVVVVLVVAVIVV VVVVVAAVVVGAVVVVVVVV MVVVVVVVVVEEDNQHKTGA INNNNTAKNPQQSPFHSPATST GAEATQMRRNQKTNPHNMTK QVSLTPPKITLAHQQWIQTKKK YLIYLKKHSGVNKIPRNPTYEG CEGPFQGELQTTAQQNKGGHK QTEDHSMLMDRKNQYCENGH TAQAVPNPYTLLSQIPEDAEWF TVLDPKHAVFCIPVHPDSQFLF AFEDPSNPMSQLIWTVLPQGFR NSPHLFGQALAQDLSQFSYLDT LVLRYMDDLLLATHSETLCHQ ATQALLNFLATCGYKVSKPKA QLCSQQVKYLGLKLSKGTRTLS EERIQPILGYPHPKTLKQLTAFL GITGFCQIWIPRYSKIARPLNTRI KETQKANTHLVRWTPEAEVAF QALKKALTHAPVLSLPVGQNFS LYVTEK\TGIALGVLT/PGTSAQ LAELIALTRAPELGEGKRVNIY ANSIGREREFLTSKGTLVKHQE AIKRLLLAVQKPKEVAVLHCW GHQKGKEREIEENRQADIEARR AARQDPPLEMLTEGPLAFELA MATARAELSLAIHHCCLPPPPQ TRCWLPSLRIRQGVCCIPDPAR AITLTAWPKIPFLGIRKAKNPRS EKTRLATILEAACCHFGSGPPPS WELWEQGPPVTVQTHILRSHL

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3401	33769	A	3438	294	2340	EKCRHNCSSRVWQSLVSQSVW ATEGQYGRTKNARPVQVK\DS ASFPYQRRYPLRLEAQQGLQKI VKDLKAQGLVKPFNSPCNTPIL GVQKPNGQWKLVQDLRIINEAI VPLYPAVPNPYTLLSQIPEEAE WFTVLDLKDAFFCIPVHRESQF LFAFEDPSNPTSQLTWTVLPQG FRNSPHLFGQALAQDLSQFSYL NTLVLRYLDDLLLAAHLETLCH QATQKKTGIALGVLTQVQGTSF QPVAHLSKEIDVVAKGWPHCL WVVAAVAVLVSEAVKIIQGRE LTVWTSHDVSGTLTAKGDLWL SDNLLLNQALLFKRPVLRLHTC ATLNPATFLPNNKEKIEHNHQQ VIVQTYTIQGDLLEVPLTDPDL NLYTNGSSFVEKGLRKAGIHPS RQWTPLWPKAGPEMLSKRQVL ESGILKAFLVPYLLVAVLGSIDF NGKPPVAVFSLSQAHRFLCAT WLLLGYGEVWIHSHTAIKTYQ RRRSQDGRIGTAPVYSSQRERR RRRVISAFPSEGIPTDLQLRVLS VRRKTNKQKGHPHQKPICTSPS SRPKVDKTTKMGKKQNRKTGN SKTQSASPPPKERSSSPATEQSW MENDFDELREEGFRRSNYSELR EDIQTKGKEVENFEKNLEECITR ITNTEKCLKELMELKTKARELR EECRSLRSQCDQLEERVSAMED
3402	33770	A	3439	2	350	YKVSKPKAQLCSQQVKYLWLK LSKGTRALSEERIQPILAYPHPK TLKQLRGILGITGFCRIWIP\R*S SPTGQE/FSLYVTEETGIALGILT QVQGTSLQPMEYLNKEIDELDQ GRTH
3403	33771	A	3440	1	897	
3404	33772	A	3441	1	429	

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3405	33773	A	3442	3	957	NKIPRNPTYEGCEGPFQGELQT TAQQNKGGHKQTEDHSMLMD RKNQYCENGHTAQAVPNPYTL LSQIPEDAEWFTVLDPKHAVFC IPVHPDSQFLFAFEDPSNPMSQL IWTVLPQGFRNSPHLFGQALAQ DLSQFSYLDTLVLRYMDDLLL ATHSETLCHQATQALLNFLATC GYKVSKPKAQLCSQQVKYLGL KLSKGTRTLSEERIQPILGYPHP KTLKQLTAFLGITGFCQIWIPRY SKIARPLNTRIKETQKANTHLV RWTPEAEVAFQALKKALTHAP VLSLPVGQNFSLYVTEK\TGIAL GVLTQELVLSWQN
3406	33774	A	3443	146	1303	EKCRHNCSSRVWQSLVSQSVW ATEGQYGRTKNARPVQVK\DS ASFPYQRRYPLRLEAQQGLQKI VKDLKAQGLVKPFNSPCNTPIL GVQKPNGQWKLVQDLRIINEAI VPLYPAVPNPYTLLSQIPEEAE WFTVLDLKDAFFCIPVHRESQF LFAFEDPSNPTSQLTWTVLPQG FRNSPHLFGQALAQDLSQFSYL NTLVLRYLDDLLLAAHLETLCH QATQKKTGIALGVLTQVQGTSF QPVAHLSKEIDVVAKGWPHCL WVVAAVAVLVSEAVKIIQGRE LTVWTSHDVSGTLTAKGDLWL SDNLLLNQALLFKRPVLRLHTC ATLNPATFLPNNKEKIEHNHQQ VIVQTYTIQGDLLEVPLTDPDL NLYTNGSSFVEKGLRKA

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3407	33775	A	3444	1	1647	MNKEDYNDDDDNGDIKYLPDI KTGYNKTVQIPITSENSTVGLSN TEADEMDRLKCERDDALKEVN TLKRRTKGGKHLTLKVTYTLSE TNLHKNYLWECILMGQLGCYE ILRKPSPALGLTPEHKGNVGHT GEKTGAG/PATSRPPDSFPN**G PPFNPNGTKGDRQRGKQQTKE CQYSPIMPTPSSGRRRIWSSQ\R HVPFSLSDLIDLAVPNPYTLLSQ IPEEAEWFTVLDLKDVFFCIPVH PDSQFLFAFEDPLNPMSQLTCT VLPQGFRDSPHLFGQALAQDLS QLSYLDTLVLQYVDDLLLAAC SETLCHQATQALLNFLATCGYK VSKEKAQLCSQQVKYLGLKLS KGTKALSEECIQPILAYPHLKTL KQLREFLGITGFCRIW/NFQALL LERPVLQLCTCATLNPVTFLPD NE\EEYNCQQIISQTYATRGDLL EVPLTDPDLNLYTDGSSFVEKG PQKAGERRAVLASQTSLTPLGR NGRSIPATLALESKELVKSVRA LLDMDCAIPFLVGTSIVDPYLK YEPTTKNHLIMVQGEKNCITGR
3408	33776	A	3445	1	2217	
3409	33777	A	3446	1	749	MNQSDQEMTGAFVHMKSYTG LISGVAVKMERHIYQDRRIAIEK EFNSCRTGCMGDWSFTITQIRL LENTGIRVFKDNLVEEAEWFTV LDLMDAFFCIPVHPDSQFLFAFE DPSNPASQLTWTVLPQRFKNSP HLFGQALAQDLSQFSYLDTLVL RYMDDLLLAAYSETLCHQATE ALLNFLATCGYKVSKPKAQLCS QQVKYLGLKLSKGTRDLTTFLP VNEEKIE/P*LSTSNCSKLRCSRG TSRGSLG

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3410	33778	A	3447	1	1374	MPLLQMIATPLQQSLISTEDEM DELTEVGFERWVITNFTEEPSPA LGFTPEHKGNVGHAGKGPLESS SPDPFLCGQEKQEKGAGLLHRQ YPLRLEAKQGLKKIVKDLKAQ GLVTPCSSPCNTPTLAVQKPNG QWRLVQDLRIINEAVVPLYPAV PNPYILLSQIPEEAEWFTVLDLK DAFFCIPVHPDSQFLFAFEDPSN PMSQLTWTVLPQGFRDSLHLFG QALAQDLSQFSYLDTLVLQYM DDLLLVTHSETLCHQATQVLLN FLATCGYKVSKLKAQICSQQVK YLGLKLSKGTRALSEERIQPILA YPHPKTRKQLRGLLGITGFCQI WIPRYSEIARPLHTLIKKTQKAN THLVRWTPEAEAAFQVLKKAL TQAPVLSLPTGQDF\SLYVTEKT GIALGVLTQHYGEERNS*LPTE YLSNIRKPLGDYYWLYRNLKR WQSYTARVIRKERKGK
3411	33779	B	3448	1	2862	
3412	33780	B	3449	94	1248	
3413	33781	A	3450	1	3805	MQWEEAEKDPSGSCVFQRPPV ALVFPLHSKWTLVNSPPSSGDP YVPGRPAQSGQLSLSPAPPYVL PGPGKIKQAGNNPSLTSIYRSEV FCAHRHLHPPQLVCARGHIGSA HLSVDRGSLIWEVLESTVWART NEWSPVTRTVLISALASTHIPQP CESRPPVPPEYEVTVLRSQGTA QLPPWSSSTSWRLTDPSCPKHA AWLTDLASSKGPAAGGTGSFS QPGTLTSTRTNPLKKEKSPEDL KQIKIDLGKFSDN
3414	33782	A	3451	1	444	YSLVEFHTLVLQKSDVEAVF/S KYCFIVGCSVHKGFAFV*YVNE RNARAAVGGD\DSSSFDLDHDF QRDYYDRMYSYPAHVPPPPIAR AVVPSKCQHVSGN\RRGKSGFN SKRGQRGSSKSGKLKGDDLQAI KKELTQIKQKVDSLLENL
3415	33783	A	3452	3	93	
3416	33784	A	3453	117	316	SSATFSAL*ETLPSNTMASSSFD LDYDFQRDYYDRMYSYPARVP PPPPIARAVVPSKRQRVSGNTS

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3417	33785	A	3454	102	1059	ETLPSNTMASNVTNKTDPRSM NSRVFIGNLNTLVVKKSDVEAI FSKYGKIVGCSVHKGFAFVQY AYE\RNARAAVAG\EDGRMIAG Q\VLDINLAAEPK\VNRGKAGV KRSA\AEMYGSVTEHPSPSPLLS SSFDL\D\YDFQRDYYDRMYSY PARVPPPPPIA\RAVVPSKRQRV SGNTSRRGK\SGFNSKSGQRGSS KSGK\LKGDDLQ\AIK\KELTPD KTKKWDSLL\ENLEKI\EKEQSK QAVEMKNDKSEEEQSSSSR/VK KDETNVKMESEGGADDSA\EE GDLLG*MNDNE\DRGDDQLE\LI KDDEKEAEEGEDDRDSANGGG
3418	33786	A	3455	299	509	
3419	33787	B	3456	16	101	
3420	33788	A	3457	1209	1828	GNCDSPARPARPPHRQGCPRPS PPPRGRPRALGPTRASAARAPA DLPPPAAPHPAPAALVPHTAAP KA\RNALPGSPGALTEGAVLLP NAGARPRRPRSSEKP\GPAPSWP RIPGFRTGAPPPATPVLAAGGL APPSPGLAGQQVALPSQVPADT QSGVKSGSQDRGRN*QSAGSA GGGARTQVPGPLRMWKRAVW PGDWAPHPANI
3421	33789	A	3458	387	772	PHRKQAEPPRHHERLGRRVRH HARHGRGSRPDTAAEAAGGCG DPRAFQQLERRLRHPPLRWQGL LRRQRLLREEPRRSLL/QTS*S*C SPVTRPSSGCSSPRSWMETRRG APAPPAPRSRNKPTTWWPH
3422	33790	A	3459	362	608	FFFFFLNRVLLCHPG/WS*SGNH QWQSWLNS*PQTPGLK*SSFLC FRKWWDYKHEPLYPAKPHFEF LFGSSLQVREFFGKIKV
3423	33791	B	3460	1	612	

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3424	33792	A	3461	1277	2152	SRAAPTCFSWLPCGASTCPWL MWAMSGRMVAPLQRVLRAAP GLEGTLGGRQHPGTPPSVLHFS LTMNSMFGLQDFNVTPLAAQA TLPPGSPGRPTLVPSTAAPNSLQ MFTGGHGA*FPRWQPQPPSGVS /SHGAPPGVPHYCRQGRSPGKR\ QRKWLESEVQAQGP*EPDPTQL QTSTRTACG*GPPSQADPDPDP TRPRTPDLDPNCMRLRTPKPGR RQSRPH\GPRTPTQTDPDPPVQP PAPEVKPQRPP/WAARAPSDTA AS*GGLTCNSRPIREGQMGSPSP AGSLLLGAL
3425	33793	A	3462	1	2064	MDGQCSHYCVKTDLRVHSPFT TGAVHADQSCCKTTSARWEDT CDLTGSKKTLVISNIVIRTRSDD KLENEWETQSQNRNRVKPTAA DPCRNE/NEHSS*EKHPEVLQES ANDRLRDNERVSQRQSQPTTVS QRQSQPTTESEPTTES/RQRQSQ RQRQSQPMTESETMTELQKMT ESANDRVSQRQSQSQRQSQ\QR QSQRQRQSQSQ*QSQSQRQSQS QRQSQ\QRQSQSQRQSQ\QRQS QRQRQSQRQ*QSQSQ*QSQPTT ESEPTTEVSQRQNQRQRQSQP/ DDRIRDNDRVSQRQNQRQRQS Q\Q*QSQRRQSQSQRQSQPTTES EPTTESANDRVSQRQSQSQRQS Q\QRQSQSQ*QSQPTTESANDR VSQRQSQSQGQSQSQRQSQS/D DRVSQRQIQSQHQEDRPPKYQN KNVQVHA/DDKPRSDPQRRRNL TPPVKTAERRPHQEHVVKGEK ATSPSRHSTSTAPTRPPSAETAH VNVMCGGDMAHINQGHVEAP QGSHEKHVGAARDQYERRDA QSEKSQQVQTTGLRVHVSRRPP HDGSLTSTGLRVHVSRRPPHDG SLTSTGLRVHVSRRPPHNGTVT STGLRVHVSRRPPHDGSLTSTG LRVHVPRRPPHDGSLTSTGLRV HVPRRPPTTALSHPLDVSICRTL NAYPEMLTGERSTFPCVNVKN EKAVESKKDTPFKCESKESWI
3426	33794	A	3463	1	424	

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3427	33795	A	3464	1	492	MDESSFRGSITQSGSAKTAGLT GFCKLCKTSSWHTGAAQILEGG MEKANSPQYADPQTHLSWHTL PPGSQATSANESNVNFLSLPDT NSPEIRPDHSPPVPDRSVSPLEHI PRTFPKPGTG/PPHINTVTNPSA GAPR*E*PS*SGFNPGCFQLVRP SRISGTPV
3428	33796	A	3465	107	543	KREGWKEESDFWDGSHLPPLN SRCSTRKGRKTGRCGAATAAA SSPREGRRPPPSWAGHPCLGSC QWLRSCR/RGLAMAPGALPAL GEEEGPGASGLSAEL/RASERGL GQGLGPAALHS*ASPTPWAPVR PEPPRRAPPPAPWRPVPL
3429	33797	A	3466	27	1021	STQTWPVSEETGSPPQRNRC*SS HQPDTASWVLQREYSHRKGTA PRGMQGTLPLCPSLSGCRSPSCP AAARPPRPRAVRFPPPATAAAS SPREGRRPPPSW/RRPSLPRGLP VASELPEGLAMAPGVLPALFGS TLPL*AVT/PH*ECL/PASLLKPA RP*THREK*TTPDVQP*EL*HSP *RSAASLQEGPQLHS*SQ*DQEP TNSGHTYTLGTGR*FYTVCQFL WLG*TYRSSHRPGFACRCLEPG SAAPCPSHCLSAGPEGTL*AAC LGKVPGRSAPRSDQWSPGGRA PRGVPPPPLSRGHCKALASCAP SADA\REPPHRALLGSPKVHTP
3430	33798	A	3467	807	1428	GSDRLQPQPLLFGRDVLLLLPS GPAIPASGLASVFGAAGRAGHG SGGSA*TWGRGRTRRERPLGG AGASE\PGSVGPRGA\GWVSGP VRAPPRAAPGTLAPSSGRCRAP PPRRAQACVALTCPGPGGRCPL PMDRPALAMP/SHL/HPRPGQV APRWSPCSRRREEKGRHERVDI GHSHLVFALTLFLP*FGGGGKT EAAQNSWRIPPAG

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3431	33799	A	3468	68	1153	LLKMFRAKAACLTSMAWVLPP LSLIVLVILSPGSFILQITFTLLEP VLRRPSSAEKPLEPGPSSSPSSG RARGA\RPALPAAPKPLASPEA GMAVPGWGRR\SPSRREEAGA VACLSLTVFSGKWICQQAP/SA WGCCC*D*GKLVHRST*RCAR* KYPGLKPDQEGYCQPGAPVEV HPRCRDFPS/VLRRNLGFSALAQ SEYLW*DHS/CVLVVG/PVLFC* TLFASFPIRLYPEELLA/HKVTQ CPSLVSPCNWLSAGGGRKFEPA LRRPSSAERPLAPYPSSSPGAGR APQPWPALPAAPKPLASPEAG MAGPGGRRTTSLPKRRGCGCS RPASSCFSSLSGWAARVERRQM ASIPEIALLFPSPL
3432	33800	A	3469	1	248	FRPAPIPSSAPRGPTEPVLRRPSS AEKPLEPGPSSSPSSGRARGAM ASPSSSSEATGKPRGRDGSPRM G/VGGRPSRKEEAGAVAGGGK RTARGLRGRGGPAATGQEGDR HPYRWRRQRSGILHEF*AASGF PPPPNHGRHTVQAEPPEPWPAL PAAPKPLASPEAGMAGPGGRR TTSLPKRRGCGSCCRGEAHSPT TARTGEDAPRPGREETGTQTGG DRRGAA/RGSP/RSPWA/CIRAPL PSLGVAPG/VPSGRLAHGDILISP CTLPHSELGSPGH*TQANFL*DP GRRRTVLWKVFQGRSRKG*EG RGPGRGHNYDGSVTPGNFIA*S PS/PLPLPPSFTWTLPKTRIPECS GVTKCSGTLGTRVW/RPGSWG LHPGSAPP*LRRPSSAEKPLEPG PSSSPSSGRARGAMASPSSSSEA TGKPRGRDGSPRMGEEDVPPE
3433	33801	C	3470	365	589	
3434	33802	A	3471	1	465	MVTTTCYCKKAKPIPRRCSAKE WSCQLPCGQKLLCGQHKCENP CHAGSCQPCPRVSRQKCVCGK KVAERSCASPLWHCDQIKE/CR SQSCS*RRKTKTTG\ELEAFENR LKGRRKKNRKRDEVAVELSLW QKHKYYLISVCGVVVVVFAWY ITHDVN

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3435	33803	A	3472	1	444	YSLVEFHTLVLQKSDVEAVF/S KYCFIVGCSVHKGFAFV*YVNE RNARAAVGG\MYSSSFDLDHDF QRDYYDRMYSYPAHVPPPPIAR AVVPSKCQHVSGN\RRGKSGFN SKRGQRGSSKSGKLKGDDLQAI KKELTQIKQKVDSLLENL
3436	33804	C	3473	190	265	
3437	33805	A	3474	144	316	
3438	33806	A	3475	3	342	
3439	33807	B	3476	180	1370	
3440	33808	A	3477	102	1054	ETLPSNTMASNVTNKTDPRSM NSRVFIGNLNTLVVKKSDVEAI FSKYGKIVGCSVHKGFAFVQY VNERNARG\AVAGEDGRMIA\G Q\VLDINPGLQSPKVN\RGKARC ETDLQAEMYGLLF*PWTYDFQ RDYYDRMYSYPARVPPPPPIA\R AVVPSKRQRVSGNTSRRGKSGF NSKSGQRGSSKSGKLKGDDLQ\ AIKKELTQIKQKVDSL\LENLEK IEKEQSKQAVEMKK**SQKEEQ SSQLR*KKDET*C*RLEVLKGG AD\DSA*GRGDLL\DDDDN*RS GGIDQLE\LIK\DDEKEAEE\GED DRGQRPMGGDDSLST
3441	33809	C	3478	216	350	
3442	33810	A	3479	1	3048	MGLMVLNVENCSSFGWIGRAP PRNTTVDLNSGNIDVPPNMTSW ASFHNGVAAGLKIAPASQIDSA WIVYNKPKHAELANEYAGFLV ALGLNGYLTKLATFNIHDYLTK GHEMTSIGLLLGVSAAKLGTM DMSITRLLSIRIPALLPPTSTELD VPHNVQV\AAVVG\IGLVYQG\T AHRHTAEGPVGLR*DGLLFLKC NTALTGSHTP*AAGLALGMVC LGEQGPCCGVWEELGERETFK DLIFNRKAPEGSNAT
3443	33811	A	3480	173	422	AAAERGAEEASGGAPPGILEDA GRERRGSGGGR*AGPVGDSKD GVGAV*PPQPHSHRDHHQ*PGP LGGPGCSG*PHLREGLET
3444	33812	C	3481	241	426	

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3445	33813	A	3482	3	826	RGEEAVSGKAGPDSPRAVLRG QGQVWGAAAERGAEEASGGG TQGEGGREVFDS*GTCSLGFPS* PGEQLMGLVYTLGG*PHSHRD HHQ*PGPLGG/HGCSG*PHLRW VPVSALGGRGVGADQLVRVAQ GSPETPCSLSGESWPA/GLPGPT PPGWQ**PGP*RAPGLQKAPKG PSYQQGPAPPSHRQSTAQRGVR PRTKRCPSLGCGDLSLLSLAVP VAQPAPRCAYRMLPLLFLLGRL TPVPSPLSSDKVIYNLHLQFIVF TSIKFSATPFKKKKK
3446	33814	A	3483	135	396	LCWLQIHRQGRKPCSPPSLKG* *ATCMPPRRRKGGFLSSVSMDII THSPGNEKIKMPPPTMSKQPGV LQQDCREKLSHCLVCSSLG
3447	33815	A	3484	256	1860	RAPETPRKILGEAGGCRGDGDR PAFQPVRNSRPFLSKLLGQCGR STLCRLCFRSLNHLFWLFPGPG WRGPGGHSTEDGSLQGKAGQD FSC*NLEISFFP*PSPTCSPTLHC GQKPRAGQGHLHSV\PGAPCW AEVPALLPRRVGD\PGPDILPPS TRV*RCPLDRNSPILL*VHFLKD RATTQNTARPPMGWRPLQQSR QISPAVGGKLCSLPVMI*ASPHP SASVVGETPA*IGGWGW/P*GF QLIG/LPHVRGTQPGLLESRVPS VRGTQPGLPGLPESRVPSVRRT QPGLLESRVPSVRGTQPGLPGL PESRVPSVRRTQPGLPDARVPY VRGTQPGLPGLPESRVPYVRRT QPGLPDARVPYVRGTQPGLPGF RPSRVPRSFCEGDAAGPPRRPRS YVRGTQPGLPAFPSPAFLVRVP SLRGTQPGLPGLPESRVPSVRRT QPGLPDARVPSVRGTQPGLPGL PESRVPSVRGTQPGLPDARVPY VRGTQPGLPGLPESRVPYVRGT QSSLPGLP/GVPRSFREGDVAGP
3448	33816	B	3485	111	258	
3449	33817	A	3486	1	4455	

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3450	33818	A	3487	1	2302	MTECLDRFIDSIAAVPRSTKSTV QKCLPCLSDGEDKIPDLIAITWT PRQGELLEKNVISETGTLLPTPC LDTSTKETADKSTSGKTIHQSIK TVLKDLSGSIDDLPTGTEATLSS AVSASGSTSSQGDQSNPAQSPF SPHASPHLSSIPGGPSPSPVGSPV GSNQSRSGPISPASIPGQDPGYG NS/DKSMGHEYSQR/SFLEDRFP IAVWWPRPLRLKNCLSVLSYSS PSEVTPHPKSESSGTS/SAAQDL QGCSQDVGQPASSSGGSTREQS TSSFIRIVAASSPSSCWKLQVLL SG/AGGDYSPVLLIGGYSRVCLP Q*SDASAATREP/GQNPVPIPP* ASHQCHRKEGPPCRQQAGASQ MLSRD*AKQLKPSSSHTLSKHK TT/GTRKSLLFGIKKAYNFTNKY YSELMTQTRPQSTPSIPSPLPLD DAGLERSQGNVSASSFMVLGN RERGEDTTGAGFGRSRNKEEVP CTIYVGAESP/EMC*WMDHT*R KEGKGGLVGVPCV/SREHLEEW QYQLQR*ISLKTQQV*RRKSEV LLGRS/SNTAQACSCWQLTCFM AGTQRNPQMAQYGPQQTGPSM SPHPSPGGQMHAGISSFQQSNSS GTYGPQMSQYGPQDGGGDVSD VVMAIDDDGSCHLLGSAVPGA VLVTFNLLLIIVVTLQMTEPQFR EYITGDPLESTCRHASLALAVV LHQETAMTMITDSLAVVPHSG

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3451	33819	A	3488	2	1427	EEPSRREPR/PPGHAPGAVAGG AGPMARAGARGLLGGRRPPGL RL/CARASARVAAG/CGRRRAA REPPRRRVPRRPARQPRRGATA AAATTT*WASGTRPSTAAPEPT ASAAAR\RLPLLLPRRAAAPRPE PLFQLRHAGLGPDRPAARPRPR HRSAPGPRPRAQPYGRLRCVRR RSAAGDGG/EPGLAFDEVGDRG PPLTAVPAG\ADRASEAAGPPG ATASHPGPTER*QRGRSEPGHR TEPRLTPRSRQEAPQQRAPGVG RPGAPARPAAAGRRDPLSSPEL GCSARRHSSLPCPRRGRPAGL\R QRFPALEPSPRQPPARAPR\HPR TCLRRWTPAPGPRRSTRPLPRR APMPPGPPVARPGP/PPLSHPTA RAF/HGTPATRARGPAPVQCED A*DLQPAAPRPLRQRGPRVPVP KDQ*QDRGHRVKRGRGA/RRG MGWGPVCPSEPQATGRGAPAV RPALLSASTAVVSWSLQAAGSS CK
3452	33820	A	3489	1	262	
3453	33821	A	3490	411	1919	RSYGVRWRRHAPPGRRSSPRIG KVKSASRAWRLRCCGCRRPSR TGMRWQMRWPMVTLARQPFW RRSVSWRGAWGSWRKSWRRS RATRSCSMTATASCSCRLSRID DISNYEVNLEPGGHDDITSCQG RGRSLPQRAPIGLCCSLGGGAV LADTPLFLPRPKPRDGPGSRAF QKRQQQQSALRVMQRNCAAY\ LKLRHWQWWRLFTKVKPLLQ VTRQDEVLQARAQELQKVQEL QQQSAREVGELQGRVAQLEEE RARLAEQLRAEAELCAEAEETR GRLAARKQELELVVSELEARV GEEEECSRQMQTEKKRLQQHIQ ELEAHLEAEEGARQKLQLEKV TTEAKMKKFEEDLLLLEDQNS KL\ARLGA*GQLGKWGWGALV G**MVNFTPWGLPHCGSQERK LLEDRLAEFSSQAAEEEEKVKS LNKLRLKYEATIADMEDRLRK EEKGRQELEKLKRRLDGESSEL QEQMVEQQQRAEELRAQLGRK EEELQAALARRQRFQ

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3454	33822	A	3491	3	266	KMRRLIKSKKDI\NRERQKSLSL TP\TRSDSGEGFLQLPHQDSQDS TSVGTNS*E\DGQTQHPRPI*DA QSSVCCAGSQHGM*ANHSQE
3455	33823	B	3492	1	241	
3456	33824	A	3493	1	1486	SRLHKLCNKPRRSGTTNAKRV GPDCHPMGREGAR*HHALRGR RGEAGTRGGRQRRREQDWREA GPGPRAEVGRTAASARRARGS APGPRGPSRGRSRWNTGQPRR NRGRGAERPRMQRSRPENGAR GTGAGLRGFQPRRHPGFPSRV* GSKDIPAARRRVETCPGPEPRPQ PQLPPRPWKGGGDARGDPKFP QAPNAVPGFCVIPAGGVLGAPT AAGLRPTGDVALRRPAGSVEPS GS/AGSQSQCLLCGPVPYRQQT STGP*PGGWGSP\SDVPCSALIS GTGC/PKAQHVSGSLSQRSLSL VDFGRPAS/RGSLFPWPLGTGG KS\PAAPSPQTLWQSS/P/GFLYF PGE/RKGKG*SGPGAGCEP\PIA VGCQEQPRGAEGNLPPKPADPC AGTKQPRAQRGVQQGTSQ*PST VVMTSGRGAHSRGGPVRRGAH SREVPAAVHGGD/GLLVEGHTA GRVQQPSTGG*PLVEGPPAGEG PFAEGHTAGRSSQLSTVLTTFLP
3457	33825	A	3494	3	393	
3458	33826	A	3495	145	1089	VYRTEFLQDRNYFFLSLVVSAP RTVPGTWTCLLSE*RNE*ILGCD SLFPKAGQAP*VAHITLGFQSSE YSKWKFTNSPTFLELLEEFPSLQ VSAGFLLSLLPILKPRFYSISSSQ DHTPTAIHLTVAVLMYHTRGL QPARATLMSTHSSSHPEGPLPA AVSGAQCASGFRLPEDPSHPRV LIGPGTGIPPFLSFWQQRLHDSQ QKGVAGGFPGVQGGRMTPVFE CRSPNEDHIYQEEMLEMARKG VLPAVPTAYSCLPGKPKVCVQ DILQQQLASEVLRVLHKEPGHL YVCRAVCMAWDVAHT/L/KQL VAA*LNLN
3459	33827	A	3496	292	478	

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3460	33828	A	3497	87	992	TACGFIACIG*QRLEYCY*DHK GKQQEVLSKHLQMAMDISHIR RNVSCSGRNKASSKAYGTGGS QGRACDLGHNF/TTPSSWERHC TLTSQGVDDFLNAKATFKIFDF SDAFVLSKVGFSGILIQKDENKE ELSDKDIYMEAGIFVSANRGPG VDYCGNRGLSIQGHGGWTLRP SILVSPGVEVRGNEDSVDTAAC IPAAPAPAPTLAERCTGTAWVT ASEGASYRPWLLLHSVKPVSPH STSLETWEPPYIFQKMYENAWC PDRRLPKKQSLMGNLYLGSAE GKYGVGAPTLETTIMQTPDS
3461	33829	A	3498	1	382	TADCAKPVPLAVVSLDSRYGQ WESRSSIHARH*LNSSSSSSSSSS SSPPAVYPRFIEFIHFDIQSTGQK SHRVNTRRGP\RDALF*LNSLIP LVRTSSKSAARRRP\GEAPRGTA VPGADPAGGTRPR
3462	33830	A	3499	229	367	
3463	33831	A	3500	233	525	WYFPAGRAGPADPGPGPLAGT PGAGAGGLPTYSTPLRVSSPVP RLESSSTG\SSFPADSAKP\VPL\A VVSLDST/RRDSGNSRSFHSWG VIN*MTRHLVH
3464	33832	A	3501	386	729	TGRGCCLPCTWRIRAQTCLT*T QCC/SCPTTYPGGGERRERERK RRGEKEKQKVLRKYKEAMSNK VCKYFDEGCGSCPFGENCFYKH VYPDGRREKPQRQKVGTSSRY WAQRSNHF
3465	33833	A	3502	63	559	HSSTCECT*DSRCGCKWRSAKQ FESKIIKSCPECRITSNFVIPSEY WVEEKEEKQKLILKYKEAMSN KACRYFDEGRGSCPFGGNCFY KHAYPDGRREEPQRQKVG\TSS RYRAQ\RRNHFWELIEERENSN PFDNDEEE/ALSPFELGE\MLLM LLAAGGDDELTDS
3466	33834	A	3503	374	656	RRVGCRCFHPSQTGTCT*RPPW NVHH*PATCHLAYNRHSWSPH RA/HWHIATAIQLSAHVF/ACHY QQLHHYHQHHHHHHHYRHHH HHHHHHYCHHH

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3467	33835	A	3504	1	1337	MQLQILTIFLDLHHNTNICNELE SSNVDDPCDIWEKVHISLIFTAK GSKIPKSSDFQADRELNMFDIIS QYDGCPGSIGLTSGAGSTHHRA PWTQTYPQGPTHLSGSPGCILA SITGRVTKMPESSESPAWELPRF TELFLSIKDEWTCIFLQLCCPTM LLSGFPPIRIEPWSPLSDQLNPIP LEAAIATHSRIHHCPLVFTASLP GPLTAGNQMADRLVATAVSNA RHFHNLTHVNASGLKCRYSNT WKAAKAIIQRRPTCQKRKIK/PD QEQPVQPV*AEGVRFWREDH*P /SHIRSRHSRMTSVSRRQSTWW LPSVTWT/CPTTEALEYGSGAC LGCPISGVSKGNKTRSGAAGFH /SPAFKSALCIWRFKQQHANRP YVCWGMEHRSPYSLLPRSSSSS HPQIHGNLDSDDLQVQRGECFI CRPCFHRLRSVPDTDTQCPQPR
3468	33836	B	3505	1	1158	
3469	33837	A	3506	35	369	
3470	33838	A	3507	345	564	PCASRTPVSSPWPV*PQPTSARR SPRCLPMVQ*AARASHDSQLCS CRFCVVVTPCAPQGQTCTRQV CARVTHG
3471	33839	A	3508	437	946	SFSSKIVQRMSSSCTENMHMSP SAPSSPQRPGALSLS/RPSGVGG LLKDPIAPC/SR/RLPGILSLSPQN PRAASPDSPAGFWDSVLCTCRL LRVACLCAVRSPRPRLCTRSCK GRGSSMVR*GGGLPIFSSSFSAT SLQLSSETVARVTPADECPAESP LPSHGPVSCQGIT
3472	33840	A	3509	1259	1497	KSNMSLLMVFSISSGITVTMCSS WGHLQCRQIFLSLEGLMKTSRS GPWAVL/RGWFSHT*ALDEDA ALGHPWASTRKQAPS

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3473	33841	A	3510	268	1278	SPSGPSSSHQPPALKGQVLQCL LSP*ISLRLNLHLWDVYLVEGE QVLMPMACTAFKV*WSKSTCA QWHWAFLLCLFFLLFLLDSKK DNRPPVLRAGAQCMCTAHVEV LPD\PSVFLSAKPRQGSSAARAV LASRGRKALCSG\IHVPTPSGLG CGGPLVP**FQTELLSSCPF*MC PGQPSCPAIPDTLENAVQ\EEAG PVKAMREKGEHGIPAAQPASS\ SPGSLVPTCGTVSPSQGTIRRPR GAWPRPQPRLTPLLSAPPWMR HLH/RSLWVGTISQEDQLATCW QANHTVEGAEIGFHCTKPQCGR GFAGPQGLGSATSTWNVLSSLQ ASRSIWDTAH
3474	33842	A	3511	1	1557	MSRISDDCSELCPLKAIKKERR KEKKQEKWETYRE/REKRQRG QRRRNGERKKRKNTKKR*NAG REGEKKRQKGKTEERKRRGGR RRRETKEEGGS*RNKKQA*SEE KKGRTGKNRKERRKEEGREKE RK\REKDRRGGRQKNKTRERD WGGEQQKTEREEEWARKRWK VPGGWEREAPHRELEKNEQLD KHSSSRAKLYDAGQLDLCSNLI QSCDPECPMQATSLTRYPTTTQ IFLRGAQGWVCVELFRSYGVE DTSAWERDMRNFGCMTREKQ GKPGQLLAHRHLCAHQKMSLL CADNSQKGCLSPANAAPCYGV QVAILTSAPTCPYHLEPLCRSFS LSDQQEAISDPRTAVRIARSGAS SNPRLCVTLTFPRVLQPFPHPPQ RWGEATKGGRLPAKGSPARTA AGRCGRSAGMPPDARAIFTSAA ALPKSRLVPSNIAFKGKRKDLS TKAAAPNLLALRYPRPSAPVGG SHAPSPGQQLQPEEEGNEEEEE EEEGDRAPVFTTGRKDRDSLAE
3475	33843	A	3512	1	525	
3476	33844	A	3513	69	707	LRQNQHEVLKDPRTHTHGGQM GTSSPEQRSTASGAPGWRATSS CVLLASPHHVHHAHGSQEAAS TPPVPWTQREYHGWPPGIYPFS SHLHK/RLLPNPAREEL*RRQQA PWKRHCWRDVTTPESTKNLVE SSMVNGGLTSQTKENGLSTSQQ VPAQRKKLLRAPTLAELDSSES EPRTAVHSSCTAHRCSAWCLA VSAVCPSRPCQSQRGLALS

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3477	33845	A	3514	81	446	TQGGRIKRHLGTSASPTGIMKY PPYCTCPCFQSALHPVPGGLSG KEAESQ*LSPHHPSSQAPGEDPT P/SQP/RLPKHSTLPALGFPATCG R\SPSPKPALPPRGTAPAPPHRY CCYYFPNRSHE
3478	33846	B	3515	58	1034	
3479	33847	C	3516	1	1470	
3480	33848	A	3517	1	606	MAGEDETPVPLPICGTRPI/DAA AAHMAPVPSHLRKHQRVEVHG FCQVQPSYGPGEDRGLADRGST DEHNPGAAQPRAAALHAHPGG VSQLPAPAH*AGQPPPTEPQLP VSPA*SNPQVSAPSLSPKQLPSP GS*DPAVPGLAE*K*TNSCPRD YTAVAAVLGSAPAAPAQLHPA CTLRAPSLRALQEAGAPQPPMG GSGQR
3481	33849	C	3518	76	1275	
3482	33850	A	3519	1	508	MTRQLSNCWVAAECCDPLRHV TQQVLQEAPIVSQAVGGPSRTN LATTPGSHRSTYCLSGAVSSRN LIEPAGEEAGATRARAEEPPGR LRAPSGGVPSPRPLCCRPPVAG CGSGLKMDEDGGGEGGGAVY CNLELKASGVILAVAAEKPSSG QAVLTNTEHSEPSHLKGKSSEK SYLHATPKEDIASFIAFLNVYKQ QGPP*APSYSTL/PPPPSPPPSSSI LRPLPQPATGGRQQRGRGLGTP PEGARRRPGGSSARARVAPASS P/DGLDEVPRRDSSGETVSRTM AARGCGQVGPAGASYSL
3483	33851	A	3520	451	487	SPLEKSWPGTSHTWFP*SRP*NP GRPLPDPLPADP/LRGVPPPNQR KGMSESSRALITPFHPPLTPAPL *NRPFLWSLF
3484	33852	A	3521	1	758	TPRAPLCRGAASAARS\CKWAP WPSRPRPRHP*SCAEAREGSAA QIPPASKLKHGGPSPPAA/PRRG HPRLLPAPP/VVPLPATAPAAVP SAPGKPFPTPPGLPKADPG/PIG GPLSAFSGSPPFPVH/EPTVLGSP QSTRNLPRPPAA*PPVAWARDA P\GSSPAAAAAKQTFASTQQTP KTT*EPRSPTGPAPALAKLFLTP GTCAPGQPSRKIKLPSRPVAPM GTIENIGYITKAFDWNVLFSDTT KGVRVDCMVQ

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3485	33853	A	3522	3	801	TLLMSHQKLLPLPQIKTPRSFHH SRHLHHQHRHHQKQHHKKHH HHFYYHH*NHHHHHHHHCHTPS P\HHHHRHHYYHHHHHHPHQH HQHHNINHHYHHYHHHHQHH QRHHHPSCTVCPQEE*/HNEHR KRPHRCWKVQDPR\NLGYLYIP TTHSELRLALSKHLPSFL*NKVS IYYRQSPDLCPHLNLNPHQYHH RYHHQYYHHHRRHKHYPHHH HHLHHHHHNHHHQNHHHHQE TPLHRTLGLPQGPRRRSSAAQP PPPPPPPLLSRRH
3486	33854	A	3523	3	229	WDPPPEFPGRRPRRESSGFPASI LLVTEPGARSPPRPAAHS\HPPS PLHRTLGLPPRHPDGAAAPRSS PPPPPPSP
3487	33855	A	3524	1	1257	MKAEIKMFFETNENKDTTYQN LWDTFKAVCRGKCIALNAHKR KQERSKIDTLTSQLKELEEQEQ TPSKASRRQEITKIRAELKSWFF EKINKIDKLLARLIKKKREKNQI DAIKNDKGDITSDPTEIQTTIRE YYKHLYANKLENLEEMVEFLD TYTLPRLSQEEVESLNRPITGSEI EAIINSLPTKKSPGPDGFTAKFY Q\MLEVLARAIRQEKE/VKGIQL GKEEVQLSLFADDMIVYLENPII SAQNLLKLISNFSKVSGYKINV QKSQAFLYTNNKQTESQIISELP FTIASKRIKYLRIQLTRDVKDLS KENYKPLLNEVKEDTKKWKNI PCSWVGRINIEKMAILPKVIYRF NAIPIELPMTFFTELEKTTLKFI WNQQRARIAKSILSQKNKAGGI TLPDFKLYYKATVTKIA

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3488	33856	A	3525	2	2133	WRRIYQANGK*KNK/QKKAGV VILVSDKTDFKPTKIKRDKEGH YIMVKGSIQQEELTVLNIYAPN TGAPRFMKQVLRDLQRDLDPH TTIMGDFNTPLSTLDRSARQKV NKDIQELNSALHQADLINIYRIL HPKSTEYTFISAPHRTYSKIDHI VGRKALLRKYKRTEIITDCLSD HSAIKLELRIKKLTQNSSTTWK LNNLLLNDYWIHNKTKAEIKM CFETSENKDTTYQNLWDTCKA VCREKFIALNAHKRKQERSKID TLTSQLKE/LEKQEQTHSKASRR KSRRNG*IPGHIHPPKTKPGRI* VPE*TNNRV*N*GNN**LTNQK KFRTRRIHSQILPEHSAGSSGQG NQAGERNKGYSIRKRGSQIVPV CR*HDCIFRKPHHLSPKSP*AVK QLQQSLRIQNQRAKITSSPIHQ* QTNREPNHE*TFIHNCFKENKIP RNPTYKGCEGPIQGELQTTAQQ NKRGHKQMEEHSMLMDRKNQ YHENGHSAQGNL*IQCHPHQAT NDFLHRIGKNYFKVHMEPKKSP HCQVNPKPKEQSWRHHAT*LQ TILQGYSNQNSMVLVPKQTYRP MEKNRGLRNNTTHLRPSSL*QT *QKQEMGKGFPI**MVLGKLAS HM*KAETGSLPYTLYKN*FKM D*RLKC*T*NHKNLRRKPRQYH SGHRHEQGLYV*NTKSNGNKS QN*QMGSN*TKELLHSKRNYH
3489	33857	A	3526	1	1896	
3490	33858	B	3527	1	1296	
3491	33859	A	3528	1	1095	
3492	33860	B	3529	1	1413	
3493	33861	A	3530	1	1539	
3494	33862	A	3531	1	1167	
3495	33863	A	3532	1	1575	
3496	33864	B	3533	1	1653	
3497	33865	B	3534	1	1932	
3498	33866	B	3535	1	2451	

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3499	33867	A	3536	1	2502	MTELTGIQQPQIVLFEHKGHKL VQGSSSDAGKVNRIYQHYEAS DKFNYTTGLAWKTAPEQTGKT VRKQQIKLNVKKMESRSKMQE HSSSPPMEQSWRENDFDELREE AFRRSNYSELQEEIQTKGQEVK NFEKTLDEYITRITNTEKCLKEL MELKAKARELREECRSLRSRCD QLEERVSVMEDEMNEMKREG KFREKRIKRNEQSLQEKWDYV KTPNLRLIGVPESDGENGTKLE NTLQDIIQENLPNLVRQANIQIQ EIQRTPQRYSSRRATPRHIIVRFT KVEMKEKMLRAAREKEIQTTIR EYYKHLYANKLENLEEMDKFL DTYTLPRLNQEEVESLNRPITGS EIVAIINSLPTKKSP/GPVGFTAE FCQRK\EGILSISFCEASIILIPKL GRDTTKKENFRPISLMTIDTKIF NKILANQIQQHIKKLIHHDQVG FIPGMQGWFNICKSINVIQHINR TKDKNHMIISIDAEKAFDKIQQL FMLKTLNKLGIDGTYFKIIRAIY DKPTANIILNGQKLEAFPLKTGT RQGCPLSPLLFNIVLEVLAGAIR QEKEIKGVQLGKEEVKLSLFAD DMIVYLENHIVSAQNLLKLISNF SKVSGYKINVQKSLAFLYTNNR QTESQIMSELPFTIASKRIKYLGI QLTRDVKDLFKENYKPLLNEIK EDTNKWKNIPCSWVGRINIVK MAILSKVIYRFNAIPINLPITVFT

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3500	33868	A	3537	1	2197	MNNAKENFLGRFQDGRIGTAP VYSPQHQRRRRRVISALPTEPPL VIPRQTGFGVDLQQTPTDLQLR VLTVRRKTTKQEGHSTKTPSVR YHHQRPKEDKTTKMGRNQSRK AENSKNESASSPPKECSSSPATE QSWMENDFDKYTEVGFRQLVI TNFSELKEDVQTHHKEAKNLE KRLDEWLTRINSIENTLIDLMEL KTMARELRDSCTSFSRQFDQVE ERVSVIEDQMNEMKREEKFRE KKMLEVLPRAIRQEKEIKGIQL GKEEVKLSLFADNMTVYLENPI ISAQNLPKLISNFSKVSGYKINV QKSQAFLYTNNRQTESQIMSEL SFTIASKRIKYLGIQLKRDVKEL FKNYKPLLKEIKEDTNKWKNIP CSWVGRTNIVKMAILPKIIYRFN AIPIKPPMTFFTELEKTTLKFIRN QKRAHIAKTILSKKNKAGGIML PDFKLYYKATVTKTAWYWYQ NRDIDQWYRAEASEIMPHIYNY LIFDKPEKNKQWGKDSLFNKW CWENCLAICGKLKLDPFLTPYT KINSRWIKDLNVRPKAIKILEEN LGNTIQDTGMGKDFMSKTPKA MATKAKIDKWDLIKLKSFCTA KETTIRVNRQPTKWEKIFATYS SDKGLISRIYNELKQIYKKKTN NSINKRAKDMNRHFSKEDIYAA KRHMKKCSSSLAIREMQIKTTM RYHLTPPEVEVVLETL/NH/RSW
3501	33869	A	3538	3	242	NLEEMDKYLDTYTLPRLNQEEF ESLNRPITGSEIEAIINSLPTKKSS GPDGFTAKFYQSIVLEVLARAI RQEKEIKGIQLGKEEVKLSLFA DDMIVYLENPIISAQNLLKLLSN FSKVSGYKINVQKSQAVLYTN NKQTESQIMSEPSFTIASKRIKY LGIQRTRDVKDLFKENYKPLLN KIKEDTNKWKNTPCSWIGRINI MKMAIVPKVIYRFNAIPIKLPM TFFTELEKTTLKFIWNQKRARIA KSILSQKN

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3502	33870	A	3539	281	3228	KPRLENYMKNAEASRADAINW KKGY/LVMEDKMNEMKREGKF REKRIKRNKQSLQEIWDYVKRP NLRLISVPESDRENGTKLENTL QDIIQENFPNLARQANIQIQEIQ RTPQRYSSRRATPRHIIVRFSKV EMKEKMLRAAREKEIQTNIREY YKHRYANKLENLEEMDKFLNI YTLRRLNQEEVESLNRPIRGSEI VAIINSLPTKKSPGPDGFTAEYY QRYKEELVPFLLKLFQSIEKEGI LPNSFYEASII
3503	33871	B	3540	295	2804	
3504	33872	A	3541	83	480	
3505	33873	A	3542	159	729	PTIVGVVIKFSVCISSPWSHLKP TFHATSWLADGDTDGCVLYFA SSCSSYQ*HP\CSSVPEPRYGRRI GSEFSAGSIVRFECNPGYLLQGS TALHCQSVPNALAQWNDTIPSC VAPELREECRSLRSRCDQLEEM VSVMEDEMNEMKREGKFREK RIKRNEQSLQEIWDYVKRLNLR LIVVPERDRDNGTK
3506	33874	A	3543	1	1116	MMARGAGVLIRKIYPLNYKHS AVEQVSRAYSFYTQRPVVPEPR YGRRIGSEFSAGSIVRFECNPGY LLQGSTALHCQSVPNALAQWN DTIPSCVVPCSGNFTQRRGTILS PGYPEPYGNNLNCIWKIIVTEGS GIQIQVISFATEQNWDSLEIHDG GDVTAPRLGSFSGLTPH/WKLS RCMAC/DPSERGLSCTWALVI/H KMEPEQPVCGKQHPEDSQGR/K GPGPGPQNHLLLPGF*VSDGRG RSRSELTPAGSFQWQHSPRNGV *LHQPSPAQVPQRLFKWRLLCP QFP\GDFVKYQCHPGYTLVGTD ILTCKLSSQLQFEGSLPTCEATP SSQCVWVSPHRPEARLPAHGPA PKRHVCQKASLLICGKEGMQL
3507	33875	A	3544	373	1051	RHLLGAQCLSRAPWCWNNQAS FPFPRCPRAKGQGTARASFSWL GCRIQHEGPIRVQGRRRPHRRE PAWAHLHPPMPCRQPNLRP/PG SLRVWPC*KSLC*PSPRPARTHP PGQRCHPYRVPSPPSPSPRPPS*F SRTFQPPGGPRTLTSGPRTQETL SPENVPGPGAP/PAPRHRSSGPK ADVALRMRGLSRAPPSAARKE RGSPESERPLNLSDGSGCCKHF TTVRA

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3508	33876	A	3545	1	411	RGREARNAAAVGAAQACT*FH RTQGPSRLGGVRGQLALPLRA GLGDCIFPV*AKSEFS/HSPLHAP ASLCWGP/PPHPVL/WATHRRQ DCGTLILQGSPAVSN*DSAPPAL ACRLSCGGGQGERTAPPSRCGE KTPWEVPG
3509	33877	A	3546	107	550	TFQMNSLTECCPSLRGWGAPQS LPMPALQTPGSAHLRCQGLLSV ETEVLWCHPTVIQSAVALKLH* AISPCF*LPPNYPLSGSSL\PTPH ACLSLPNLQCASPL*QPPPCPRE VAPLSLEIPESFVYGILGTHITGC LCISLVLPLSP
3510	33878	A	3547	54	825	VGGCLAGPQDPDGVFQTSLRK GVNRAQQQRRQLLPGPTPSKA KDSHP*EGG*GASPNAALLSGA GELPRACQCRLSRHLALPTCAA RVC*NPVKPRKGRSEPRSGWAS QLPGGDSRLPLRPGTSQGVFSP HRLG/EGGKLVLGVLSLSLKQR GFPGE\WGAAVLSPVRGPRTGW GE\DLPRALPDQSDGSGRMRKS AAEAETGPGARSAAGRSDSDS GGRPDSCQTVPAAR/SPPCLRRQ KLPRERLPRAPNP*GPRPLGR
3511	33879	A	3548	1	1335	
3512	33880	A	3549	1	903	MPAGYHVLSDVVSVETPGCPA EFLNIRIPPGDPVFDPDQRGDVP EPPRRVPPPAARRPIPSTTQGLR SVGARCGTGKQLHLQPQCEIH WVKPAGLLSLVGTWRTFMSSS ELVNIPIGTRYLAQAVTLTVKV CSFTAEASETTSPPGGTNNSRR AALRAVTLTAKVCSFTPEPARP RTHQKEETPNTSEHQKEQTPDT SAFKNCNTHGEGLQLHSLSPGR PPTPPGRPNNWRNPGLKSWNT YPGKVRNFHWLFSKKEIEDIRN TTLRDVLVAVINIDPSALQPNVF VWHKGGFLP\CPQFFP

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3513	33881	A	3550	1	797	ATRFGGNLVLVGLGFEMTTVPI LHAAIREVDIKGVFRYCNTTVT LTAKVYSFTPEARETTNPPGGT NNCRNAGLRAVTLTAKVRSFT AEPARPRTHQKEETPNTSEHQN EQTPDTPPLGTVTLNARVRSFIV EVNSQNPLLMWAAPDPAPGQN GPRGLYAFGAERGNREPFLQAL GLVLVRLH\NLWGQRLARQDP\ DWE\DEELFQQP\RQRVIATYQI TSPHTCTYSRTRCFPVKEIDKEQ SLTSHHYLSCSHCFGHEQSDHP
3514	33882	A	3551	23	3990	HGHFWLGHGPLWLSAPSWTLI LENTTGSRGGIVWGTRCPRKRA KSSTSPVQSLELRTPFRGRCSDL MGGTTTSWSTDG/CSKGYHVLS DLVSVETPGCPAEFLNIRIPPGD PMFDPDQRGDVVLPFQRSRWD PETGRSPSNPRDPANQVTGWLD GSAIYGSSHSWSDALRSFSGGQ LASGPDPAFPRDSQNPLLITGPG GCTQRGNREPFLQALGLLWFR YHNLWAQRLARQHPDWEDEE LFQHARKRVIATYQV
3515	33883	A	3552	2	663	VLLDERSAALDGAKRDGTLAL AAGALCREARAAQVFFLKGGY EAFSASCPELCSKQ/INVSANCP NHFEGHYQYKSILCGMTTHKA DISSWFNEAIDFIDSIKNAGGRV FVHCQAGISRSATICLAYLMRT NRVKLDEAFEFVKQRRSIISPNF SFMGQLLQLESQVLAPHCSAEA GSPAMAVLDRGTSTTTVFNFPV SIPDHSTNSALSYLQSLITTSSHC
3516	33884	A	3553	3	669	GYEAFSASCPELCSKQSTPMGL SLPLSTSVPDSAESGCSSCSTPL YDQVSRCPCHREEVRTGKGME E*CQGGI*KVTCSIIYNGGDTGI* FIPQLSGLTEPSLQL*ALRK*TC WSCPGKWA*FPIYLSSSNRTEFT RYLKLTFPAESFCGYGHWPWL *ASLMNVGYFWISG\GPVEILPF LYLGSAYHASRKDMLDALGIT ALINVSANCP\NHFEGHYQYKS

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3517	33885	A	3554	3	1377	WAVCATRVGGAVGGTAKKPR SPEPRVTLLSQSKSGFWFGAER PGGLAFPRKAPPCPWPREQTKS TAGPITLGALRPAMVMEVGTL DAGGLRALLGERAAQCLLLDC RSFFAFNAGHIAGSVNVRFSTIV RRRAKGAMGLEHIVPNAELRG RLLAGAYHAVVLLDERSAG\LD GAKRDGTLALAAGRA/LCREA RAAQALLPSKGGYEA\FSASCP EL\CSKK\STPMGLS\LSLSTSVP D\SAESG/CASSCSTP\LYD\QGG PVEILPFLYLGSAYHA\SRKDML \DA\LGITALDPNVLSQIVPNHFE G\HF\QYKSIPVE\DNPKADISSW \FNE\AIDFIDSIKNAGRRVFVHC QAGISRSAT\ICLAYLMRTNRVK LDEA\FEFVK\QRRSI/LSLPNFSF HGASLLQFESQ\VL\APHC\SGR GWGAPANAGLDRGTSTTTVFN FPVSIPVHSTNSALSYLQSPITTS
3518	33886	A	3555	450	719	
3519	33887	A	3556	63	332	
3520	33888	A	3557	573	1309	WCKGEGEATEKGPRAEAQASP LSEEAGAGRCPGCPYRDAQPLL GSGHTLKRAIQDICYGPGHYQA RAAREVHPPGRKIGKQSLRRPC KLETDDHLSRSLRELD/SW*FGR KCAGAGLTERTQGRLRRKRTL SSEGALPQVLELSAEASKRGSL GKPRKFGKKNPGHGAPQPVVF QSRQCLQRILGEHPRTRPCLRN DNPGASSAPAQATFISPSEDFSS SSQARSPALSLSFREGLVMTHG

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3521	33889	A	3558	1	1797	KDSAGPGPPVALLLPGAA/CLSP APGCRRAAPRWSSPGPRTAAG* RRMWCASASLA*SPCRPPRSRW WRDAGSGWTPHCPASAAWGA EQEPVRSWGPRASQSHCPGGLR APPPGSVRCSTQ*DCSSVRPAW SRS*GAC*QV*PRCPCRTPATG WAPPPQGRCGPTTAPGSTGPAG RASLCCPRRAHLPG*WPQKLIC AHPGAKSLGLACQPHRG\KGTP IEG/PACGT*GGRRGSGCPGRPH TRRRC*PPAPCGRRSAGSAHPA RPWPHGPGGQQRDPGPAYRGG QGGRSPASPSGRRLPASRAGRS RAARGTPGRPEPRSPQRRTGTV QPARCPWPPHRAAAGPPRRGS GAPAPLGRTRSFGTAGKAHPW PRRRPGHW*SAAAAPATGVPA CRAGSWVSAAPPAEGRPARAR RHPGRCPEASGPRGRRSAAHGH GARAGSPQPGAPPCHLPGIPAR QPLGLPRRTRCFGGIAQRGRAA RHCLLSRPSAKAKRNSSYREPG MGGWRSPQALGEYGKGSQAG SARLSGAASQGRRARHLRGKA PAWNPAPPPSPPPPALGLPLRTQ REATRKPRREEARRPRPRPLRP GGANGSPGPPRAARA
3522	33890	A	3559	1443	1871	PFVYTSSLGRPPSIS*QPFVSGSG CSCP*RSRPSGAWRA/RSASSPA PPP/KAP/SPRPGPRATAGASRRT AGPALCGRPR*GSRGRHLFSRP GGTRRRRRAAR/SAGLPAPGGS EPPKSGSGFPSSPYASSSGLIPGN RSPAAAGEL
3523	33891	A	3560	62	864	ALAESRGDLEAGPSSNTWEFW ELAGFSVLFLGNRRAALGLCEL PSLRAGVEFTAVQRLWSSAGA TWWSKLAVPLAGSAGRENPGS LLDGLLFTLENNLSRGQGAPST PPAARRAAR*DGGQSASSS\PAL ESPPERHRRLALVSEQKPQEPA/ RSSRRSCGTRLPRLVFCSKVCR RAEPGGSVTRREGGAEREAEER KRGR*GEARR/RQGGRKSTRRK KQAIKGKRESQKRRGGRQGRG RAASPPL*EPRARQPRGSAAPSL LRGLSGCL

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3524	33892	A	3561	3	2701	TGLWCRCPRSARRSVGRRPGT APAARPPRPAAQKQALGSRERV GTGPGRILRPGGWGCFP\GPRGT EDADQRAARGPVGAGTQQHG RAVPR\GPQNEPDETLLP/GGPS PRGGELRGRSGARGLP*SLTGP APGPQRGG\G*SPSPGRASSKAG PWKRPGASRASLQRASSM/PAS QVDWGG/PGGSPRCNRCRERKP GTGPGWPPRLRSPGNLRPGVGG LGLALPARTAAAAPRPRERWRS PGAPCLGAQ*PSL
3525	33893	A	3562	2	905	HEGFFFFILGCPFPNFIPPNLVSV RKLGVKPAWGAA/RPRLPLAP MPSREGAARSREMRRPRGIRRS PKEGLFHPEGSQGKSQNGADPQ RM*REPGSSKSSEPLPRLLGVH QTA*RWETGETGPAIGGPAELD AVHVGL*CNRGFPSSKQRARRR ARVWPGPKKRPPARAARMARL ASDQRDFSVSRKAGDGRFPVIG IRSGGGAATGSSSRLSVSSSAVL RKPGRTTGAVPAGGSARKGPSL APMLGPGSVRSASSPSPGHNPG AGS*ERAGLGERPRQKPLAVPA AAIDFPQSPASRSNI
3526	33894	B	3563	149	283	
3527	33895	A	3564	269	452	AGILFLSSSQ*SNARRPTHGALL GDWGPRCSPSPYANRSPSSSLA RQCRTRGSTRDLRVRT

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3528	33896	A	3565	1	1877	MDPQLERQMETTQNLVDSYAA IVNKTVWDLMVGVTPKTIMHV MINNRHAPPHGSRGLLWHWGC RWPCWPGGDAGQPYGTSILIEK KREKNQIDTIKNDKGDITTNPTE IQTTIREYYKHLYANKVENLKE IDKFLDTYTLPRLNQEEVESLN RSITGSKIEAIVNSLPTKKSPGPE GFTVEFYQRYKEELVLFLLKLF QSIEKEGILPKSFYKASIILIPKPG RDTTKKENFRPISLMNIDAKILN KILANQIQQHIKKLIHHDRVGFI PGMQGWFNTRKSINVIQHRNR TKDKNHMIISIDAEKAFDKIQQP FMLKTLHKLGIDGTYLKIIRAIY DKPTANIMLNEQKLEAFPLKTG TRQGCPLSPLLFNIVLEVLARAI RQEKKIKGSLQRVLSFLTTQRG LRRSLQPSIPFSFIILVRAMFLLS GLVAVTLGSPSAGNQSTVLSSW SLVAQQEKAVPTLPLQSARPPH GSAVQAAVWPDTLYQSCCPLA ENQTHFWMTGKCVLCWLCSL WSSGEGKGQAISRVLFGGVKRP YPFQGTLFLESPWNLAGSCPVK PALATRGQG*SSAYSTEPVIVQ RNAT*LKGKARVQLGAKKESG
3529	33897	A	3566	770	949	IRYVLCGGALR\MELLTKQG*SS AYSTEPVIVPRNAT*LKGKARV QLGAKKMMSQSVTPD
3530	33898	B	3567	507	1436	
3531	33899	A	3568	43	421	TSAHPGGEAVPS/LTTSTTWSRS SSLVTFTLMPPRGCSTGPPVTSP LCRMPRTTTMPASPVGSSIGQT STTLPSCPQRQT*PSACTGSG*A SAVRCAPKSSSSPATSSSMTTTT PGRATTTTTQTRC
3532	33900	A	3569	210	610	TRKSRRNG*IPRHIHSPKTKPGR S*ISE*ANNR\TEIVAIINSLPTKK SPGPDGFTAEFYQ\STRRS*TTT MPASPVGSSIGQTSTTLPSLAPR QT*PSACTGSGNHKSLTVKSFS QGCAGLPASLTGPLWWRC

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3533	33901	A	3570	1	718	MENAGEREDPTVGNEGEVRLA GPVLRTQDELSWEEDEANPTSY PKGADSYCHSDCQTIMDFSNFN AFSTPNTFALMNTYSCPQHPNS KQFQLPTFVKMGEAVSVFFIGL PHATPIVEHQNDLIAGSVRMQN QPKGSTLQCIILMPQRPPGQTLE DMDYYYSCFSDEKNLGTKKLS SFPWSHSKEVKATFKGRYPGSH ALNRHTTLPGTAWILLLGGELA FLTVKDGSPLALPSRPADGMRG RNKARVLSSLNLTASWG*QAQ SSELRTSSPGKRMKQTQLLIQK EQILIVTRIARP*WIFPTSMHFLP QTHLLS*THTA/VPQHPNSKQFQ LPTFVKMGEAVSVFFIGLPHAT PIVEHQNDLIAGSVRMQNQPKG STLQCIILMPQRPPGQTLEDMD YYYSCFSDEKNLGTKKLSSFPW SHSKEVKATFKGRYPGS\QPLT ATPHYLALPGFSF*VGNLHSSQ* RMEALWPCPPAQLMG
3534	33902	A	3571	719	1643	IQKRACSVSARRGLRTGRCGCT AGTTTMPASPVGSSIGQTSTTLP SCPQRQT*PSACTGSG*ASAVR CAPKSSSSPATSSSMTTTTPGRA TTTTTQTRCASTPPSPSTPGAAT AAGGPLVQGHGRHRVRVQSES HEGHPHGMRPQPHCSTSSTGM SAGPRVPGQV\ASSRMLTHTNG LRGPGGFKLPSHGVLDLQNGT GMPGGAVCCSTVRGPATGPAQ TGQRREPRPTRCPWSSVPPLRR GKKDLARRQVESKPVWPGPWE GTPWSLLLGCNLPALSLCCIGTS ADRSFRKFYFFQTRIPLLLTDVL
3535	33903	A	3572	1	933	MPEPPP\PPWAPARPKPPRRAPP PAPRRPVPSTTQGLRSAGT/PAR DWQAAPPAALSSPEPHFNLIAS VQTVMCPVGAPAGMQGSG\PK PSGCRLVLWTPG**KGSIWGTA ASMTRRRWTMRSRTAMSPGPQ RVPSAPKPSSAPCA*MEGKRSL LPA/TVPGCKKRYKVTWVAVG GPDPTREASLCQPSLLGTDQDL QSSPFHWHLRIRQKMRYRTPRP HAEQGMGEGSHCLMSEHHFEK TQRQFSPDYYPNPSSQLNVNGI KYHAKNGHRTQIRVRKPFKCR CGKSYKTAQGLRHHTINFHPPV SAEIIRKMQQ

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3536	33904	A	3573	2	316	CLSLPTPPWTPVRPEPPRRAPPP ALRRPVPSTTQGLKSAGARRGT GRQ/PPPAAPDCVAQ\SSTVHLA ARATK*PSAHSVVSSSPMGVLF LHGLDFPRMTRSQGLR
3537	33905	A	3574	3	1078	SLPPPPWAPVRPQPPL*VPPPAP RCPVPSTTQGLRSAGA/PARDW QAAPPAAQVFTLLKNIKMLPCL EKPGKFGSLVIMREFNNHMWQ VELKMPVPSDLPKGTGKTLILP ECIQAPCMKSNNA\PSSSSAPSP WML*A*AWLCRYCRASCGISSI PTASPVTMACC*RYMRWGILPI SEPP\QTGFSPAGANQRGPLAAT LSGPGGEGQSAVARLTGEKKN HPGAQYANRLSPRVGRFINAAG TTGFPTGKRAGHKKEPIPQSFIT RAARRSR*PSKASELGRKQRRP V/PVR*LLRSAQEEISAVGKTPG FCQGGNTGYQSQR\RKK*PANR PVKRLP*GGI*SLPGSKTYAVSV RCPDQKI
3538	33906	A	3575	2	969	VSTWETPQYRRPPSPS*RGSREQ PCSFSSPRDTPGENHWLSLPQR D*AGPPVRRALGAS*PHATRRP NRGGAS*PDLQPNHTRPFRPFPS KNPCFRFPEPLRAPTLVPGPCKP HSPAASGRVPPTHPGRGLGKSE G/SKEKPMRRTAAPTPIRFPKIT GT/PSTQTAADHALLGMRDQSL SGQSPGPKSPDADDQLQNRDH TETEQRISSGRSSALAPESQLQQ GCAGIHFRGRFCKAPPLVCERL RGW\PRGKRKGVCESAAQASP MSAAPCSTVPSPINHPRAEECG RTARDWQAAPLAALVRDPLDE ASWAPESGGDVENLYV
3539	33907	C	3576	1	444	

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3540	33908	A	3577	227	2141	FCPVATSASVTPVQTRCATRPT TAPSADCVSPRAAGGLPSGHCF RSEP*GKNWAPCPQPALTPSS/P SQTSDSEEHPSSENIPPGYEVVS LLEALNGPLTPSPAVPPLHVL/E RWPPLRNAPFIWQ*WPPAPRQD DLAS*PPV*/PAAVRDSNSKRVS PNPLPKTLPCCMKRKMSIPAAS/ TETQLSQRPSVQHLGEECGVTP ESENLTLSSSGAIDQSSCTGTPL SSTI\PPQKALPAAAWPSLSCPW HPPRSALTPSPPCLAPTSPLALK RRERLSLPPSLPAGPPQKK/REG LPAESPDSNFAGLPAGEQDAEA ALSSHYQPISHASKGDCKSGME QQGVCEREWGPATVQSDTPAA AVGLAAPGRQAVEGLSVCSLR PPCSSRCDGSGCSGQPTTVINIS LRRPTSPRTREDSEKPGQYPKG HTEARQMPGQKDKVAKRSRK V*EEKENGKGPIRRQ*KQAAPR QLGQAGLTHSLKARV/RGGTG G/AAGVLG/GAWAWRAPHQW/ PGLIALPARGNEGLSTRASGCG GCTGSPSSASPPALRSISRRALA AFPRGRARDLQPAMPEPPTPSV GSCAAPASPMSAAPCSTA/LQS HRPPKG*GVRAHGAGLAGSST CSPSAGSTG*S*LGS*VWWGRG EPLCPAQGL
3541	33909	A	3578	26	1141	VLQLLRWRVWSLFFLMFRCVR SFFLLTQKPSWLHPVDPAPGLQ VELPASPAPCARTPQPLGGRWD WAPWSRGRRSSGRLGLHRNLR RPGAQAWRAAGPGPCPAGRQL RPGEKSSAAPVGWHCWGTEYT FPSSRWPGC*APHCPGLAGPAG\ SPSAGPAKPTPTWNSSWPASAA RSPGSYS/PPLPPY\PLQAEGAGS GLGQPRKGLLHL*DVPAEPVLA GPLASGSIPLAAPPAGRGLLAPG PCPGLDLRLL*QLPPPSVFPTTP KTELVLGTPGHGQPHRGGHESS DSAGG/APTPRALRSGWDPSPPS SVCATPTSSGLSSTPQLPLHQRT SSSTASWSPGWGMGSC*VLVTS GAATVGC*RLPSISTS*SPI
3542	33910	B	3579	1	1234	
3543	33911	A	3580	443	865	

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3544	33912	A	3581	2	1524	CLSLPSPPRPPHPWAPVQPEPPR RAPPPAPRCPVPST/TPGAEERG RTARDWQAAPPAAPKEETPNA SEYQKEQTPDTPPLRTVTLTVT VHGFILEVSETKNPPIPDTGLQV VPKPLPRHTRGRVASSSIHHIRF PVSPSARAG/APPGHTPCQGTW QIQSSPAQGGGAPN\PLYSAGSA LVSSLVLVLQFVDPFVRS\PEHS VIARPSPARPGTWELGRRRTRP SQDPPRGPSGGPWPGRGRGPW RSKTDAAPGKA\ARSPAPGASC ELARRGASPGREGLAVGRAAG RGVASG/APSPAEGP\QAALGAP PGTHRSSSPSAQVPSSGARTESP W*P*LLASAGRPRPQPGYHAQE WRKRPRRPVRTRRRFPTKAPAR SAGSFETSTFSAHDPGSRGHPW GPKPLPAGGDRTAPPGAQGRGS A\SKAPARIHEPALRGHSGSRGG TPG\GSSALLCAKNCAPGDPGT AGVGR*SGTQLPPRAPLEPLSAP RRVRPVGSGRRREKVPRPGRPR
3545	33913	A	3582	1	3339	MSVRKDVEKLEPSDIVCGNVQ CYSCMETNLTVSQKVKHEVTV GPREGATKPNRMKGKEGRSGS LLGEGDFFKDESVMSSQGSSKD GEKRRGKAQRWKWPMQGICR QLGVAKSMEGYQSRRDQGGR GVSDKWPQVCAKKPEFYPTAQ VWANFSVTSCQSVTITQLCHGL RRLEISPARSNAMHLNPDPPGQ KQNLSPKVNDIITDIESSSGSGA GKFQVISKSDISEVLLQQMDAG HSSKDDPNEYGGWKSPRPRC
3546	33914	B	3583	1	503	
3547	33915	A	3584	1	787	MIKWVSYQGCRDGLTYGWSCS VETVRWLPEVHAADTSCLKISA CLSSFSSSYKAPSVVAQAAPPSS PHKTSSLCTTSAP\SRPSMRTTS APP*\SSAARPSI*NISS/SPESSAA TI*N*NMSSSPGLQLHDTQTRTS APPRVLNSAT/SQTTTSAPPRAR TPVPPGSPAPRPSQKNSHTGSFV VFSSTT*DISGSTGSSHGPPAQR LS*T*KAAPAPPQGSISTT\PDLN SGSTTS/SSRSSAPRPSLNNPFS* NSAVKKSAAEVNE

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3548	33916	A	3585	746	2018	THPQERGTWGNRQLFAVLPLPF YTSLETMSMGCGAVVAGQYQ KCPFFTIPSANFPWQKQEGMSG NPPRVRRHISLSRSCLTLAVPMT IRRSWEGAPFVGAQDGCRPLLP GRRALLLHLGLAPLL/GPPPPPV SPPWPPCKATWVSAGGRCLY/G CPSAPAPR\APPEFPAPPGFPAPP AASSPSTRCSRGT*SCGPGRPGP LGPAWSA\GQRGQLAVPEPLQA VLGALGLLRPLGERR/PAQAGT FSPTAPGRGAPGASA*GGRISG HSSGDIPRRGPSRGHPPLLAQGS DAIRSTLH/ERLSTRTRPSFKIKT PSPHQRPQQPHASWTPSSGTLS KPSTPCSSSSCAPRSGDGGG/EG HAGLPSQPAAGSQPAAPCQRPE AWAGGRGNRPGKPGAPQGPCF SLPRPQRSR*LPPPARQKPPFFTL LSLFSF
3549	33917	A	3586	1	1911	TIYAVNLFPILPQGDL*PFTMVT MHWGEGNGQIFRGLLDTGSEL MLIPGDPKCHCGPPVKVGAYES QVINGVLAQVQLTVVPEGPQT HPVVISPVLECIIGIDILGSWQNP HVGSLTGKVRATMVEKAKWK PLEQPLPRKIVSQQQYRIRGEIA EISAKIKDLKYAGVVIPTTSPFK SPIWPVQKTDGSTKIPGTSTSVK FLGVQ*CGTCQDIPSKVKDKLL HLAPPTIKKEAQRLVGLFGFWS QHIPHLGELLRPIYRVTRKAASF EWGPEHEKALQQVQAALQAAL PLGPYDPA/DQATVQLKLPVIN WVL\SDPSSHKVVMHKLREEV GQMTMVFTPATLSSLPQHAMM VSWGVSYDQLTEEEKTRAWLT DRSARYAGTTRKWWTP/HQSLS PATPVI/SQWA/HGHGGRGGGY AWAQQHGLALINADLATASAE CPICQQQRPKMSTRYGTIP\GKV LQKAVCDLNQHPIYGTLS/PIAR IHRSRNQGVEVEVAALTITPSDP LAKFLLPVPTTLRSTGLEVLVPE GGKLPPGDTTTIPLNRKSRLPPG HFGPLLPLSQQAKKGVYPPKKK SLYQKHALSYMSLFTAVPFTIA KTWNQPRFPSMVNWIENMWYI YTMEHYTAIKMSEIESFAAIWM QLEAI
3550	33918	C	3587	44	310	

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3551	33919	C	3588	20	328	
3552	33920	C	3589	288	542	
3553	33921	A	3590	332	528	
3554	33922	A	3591	3	1717	NVCQSHRIPEHCYDSLNVCSS* GIPEYSCCDLNICPSHWTPEHCY EGLNDCPSSNIPEHCCWGLNDC SSRSIPQHCFWGLHVCPLHRIPE HCSWVLSVSPSQRILEHCDENL NVCL*HRIPEHSRCCLNVCPSHR IPEHCCL/ESESLSLTQDSRTLLR L*GSECLSET*NSIILPPLFECLSH T*YSKTLHLGSECLSLT*DSRTS LLWSECSSYD/VENTTA/EGLSI CPSHRVPEHCYEGLNDCPSRRIP EHYRWGKNVFLSQRIPEHCYE GLHVRFSRGIPEHSCCRLNVCPS HRIPEYYYECLNICPSKRIPEYC CLVPSVYSSHRIPEHCY*VLNVS PSQRIPEHSCGGLNFCPSHWIPE HRYEGLNVCLSHRIPEHCYEGL YDCPSHRIPEHSCCGLKVCPSHS IQEYCCWVLSVCPSHRIPEHCY HCLNVCPSHRIPEH*EDSRTLLL LSECPSQRISEHCYEGLNVFPSH RIPEHCYEGLNDSPTHRIPEHCY EFLNDCHSHRIAEHCFSGLNLC LSHRILEHFRWGLHVCPSHGILE HCCWDLSVSHSH/SNSRSL*RVS
3555	33923	A	3592	3	191	
3556	33924	B	3593	58	477	
3557	33925	A	3594	19	367	AIQSWCHHVLQAQPHVELLVP RFIEELGSLVHGH*PRHRLPPAH SHVLHHCQLQLGHTLRPRHCIL QEHACG/RVRCLLQRQAGSPGG WCKRECLFLQE/VKPSVRICTVE MCTISIS
3558	33926	A	3595	55	555	NHFVAEAASCPPRCPFRLDAKK LVRSPSGLRMVPEHRAFGSPFG LEEPQWVPDKECRRCMQCDAK FDFLTRKHHCRRCGKCFCDRCC SQKVPLRRMCFVGPRAAVRGS APWVFPQGGGVFTD\NSSKCS* AEPPSSS/QFGNSEKPETMT/VSS FQ*PEILVSGWRQPL

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3559	33927	A	3596	182	696	PVFWIRNL*SMASRGLRRD*EH LKEAILAHSL/KAKRGGEAAEE ESEASRGWLVRFKGRRCLRNIE VQGETASAAGEAAAGHPGDLA KITGAGGYYTQQIFSVDETTLH WKKMPCRTFTATEEKISAYFKA SKDGLNLLLGVNAPGTYVLRS NISVFLSEEMSSDKRLTEMGY
3560	33928	A	3597	74	2521	RERWAAGPVTCQVTTWPGAAT TRVTWPMTRPATPCAVHGCSC PRSHWSQKCGQPASRAV/SPHP PSTCGSSA/APGPTPKQEAPSAL WPLSGFPN*EPGPGQPGD\VVE KATERMAAMKTEAGVPLVEV QDPVEVPSGR/PAGTCPAQPQH RTPAPCTADP/PALDTPTTTHPA PAPCPTAIAASWPAVW\LPQPG Q*PRCPRLIATCEGQTPAGEEPQ AAATAGEGR/VKASVSPAPRGT PCCGIRWVARPAFSGHRSSPCP GSQGCWA/PSSGVPEASEPRPGE QEPIFRKREFNKEIKSL/PEPAGV PRPAWLLSAP*APSHAELPG*PP PLPCPAKRGQPGCG*APWRPLP RRPSSV/PPPAWSPP/QDLPPLGS EPAKPTNGG/PALCFPPPHSLQP QDASEKTQG/PEEAPPPCLVPR WPPDSNSR*HPRRSPMSPAPHS TPGRRHLTQIPNYKTHLFP*APA RGPSPGRACTSPCPRQGLWWR WPAARATSGALSHLHFPPPTPA LPATFSLSSLQLPLHLPPHCVQR APAAAAGSRRRSRCPPSRRSPA CLTSPTAFMRSSPTS*PSRQPPW SSASTSSKRTSVSSWASSPSPSP TCSGTFPWA*RR*KAPASTCPR RPTGAACCVNWRSPKGPGRPP GSAPPTAAQRHPLCSRNQPPTL PRTRPQSPAAPSTPTCQPAGSSA LWSPSSTCLPAPAWVPVPPSPR
3561	33929	B	3598	1	588	

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3562	33930	A	3599	357	1011	FLPLGELYAEGSRMIWSDGFW AGHLHSCSHPRSSSFSPTCTYPL PPPPPWVERQGTRGSG\P*PGKR TSSPFRVSPGSNTRECTPS\GLLD CIPSCISLSEKPQNDSSSESA*KIP ASSLVTSGLGFCKNPQWSNTSC TSLSCDA/CPPWND/CCQMPVPC SWTFQPPEP*AK*TSVPYKLPSL WYSVSQRGKDSPSPAPPGPGRR AQPASRAAAAPPAVGP/SDRAA DPLSPLQAPIWAPRHQHGRSPR/ VR*GLRWLHGALRVVVILEGG RAQ*PPWNDFVRCQCHALGLSS LQNHEPNKLLFLINYPVCGILCP NAGKTARAPPLRARVGAPSLPA ALLLLLLLWDR
3563	33931	A	3600	63	660	KPQVNKSASCAQLAGPVSQRG KDSPSPAPPGPGRR/CPACQPRC CCSSCCGTADRAAAPLSPLQAPI WAPATSMDARRVPVRVFALTE ART*GRAPWAFPGDVNPSLAPI P*TCSYTELIPPVSFSFPPSTSGN SPTACLDSGVQLASPSGSRTGA TGGAAHSPARAPA/PPQPLGSR WDQGLRWLHGALRVVVILEGG RAQ
3564	33932	A	3601	202	515	FCKHEAAVSSGKAVGTRSQCR HSGPLRVAMKFPARSTRGATN KKAESRQPSENSVTDSNSDSED ESGMNFLEKRALNIKQNKAML AKLMSELESFPGSFRGR*PRGCS AAPRSKRRSGHPPPAWT/CSPR AAERS/PE*RRT*RNSDM*S*FP ARSTRGATNKKAESRQPSENSV TDSNSDSEDESGMNFLEKRALN IKQNKAMLAKLMSELESFPGSF RGRHP
3565	33933	C	3602	40	186	
3566	33934	A	3603	1	3189	

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3567	33935	A	3604	1	1821	MLKNFKKGFNGDYGVTMTPG KLRTLCEIDWPTLEVGWPSEGS LDRSLVSKVWHKVTGKSGHSD QFPYIDTWLPQWVRGQAAAVL VAKGQIVKEGSRSTHRGKSTPE VLFDPTSDDPLQEMAKVIPVVP SPYQGERLPTFESTVLVPPQDK HIPRPPRVDKRGGEASGETPPL AARLRPKTGIQMPLREQRYTGI DEDGHMAERRVFVCQPFTSAD LLNWKNNTPSCTEKPQALIDLL QTIIQTHNPTWADCHQLLMFLF NTDERRRVLQAATKWLGEHAP ADYQNPQEYGKEESPAQFYER LCEAYHMYTPFDPDSPENQRMI NMALVSQSAEDIRRKLQKQAG FAGMNTSQLLEIANQVFVNRD AVSHTGAEHSVVTGPVAPLSK KTIDIIGAMGVSAKQAFCLPRT CTPGTKDYRLVQDLRLVNQAT VTLHPTVPNPYILLGLLPAEDS WFTCLDLKDAFFSIRLAPERQK LFAFQWEDPESGVTTQYTWTW LPQGFKNSPTIFGEALARDLQK FPTRDLGCVLLQYVDDLLLGHP TAVGCAKRTDALLRHLEDCGY KVSKKK\AQICQQQVRYLGFTI RRGV\RLGSERKQVICNLPEPKT
3568	33936	A	3605	1269	2463	GVQEESSDLPTAVDSSRPDIRD QAWASVHWELYVHGSSFINT* GERGAGY/AVITWT/HVVEARS MPQGTSAQKAELIAFIRALELSE ALAKTVRQRCVSCRQHHARQG PAVPPGIQAYGAAPFEDLQVDF TEMPKCGDIRKIVTGDVNTPAI LGVVSSSPPSHIGNNITEDPELQ PILAGLSLSMYLVTVLRNLLIIL AVSSDPHLHTPMCFFLSNLCWA DIGFTLATVPKMIVDMQSHTRV ISYEGCLTRISFLVLFACIEDML LTVMAYDCFVAICRPLHYPVIV NPHLCVFFLLVYFFLSLLDSQL HSWIVLQFTIIKNVEISNFVCDP SQLLKLACSDSVINSIFMYFHST MFGFLPISGILLSYYKIVPSILRIS SSDGKYKAFSTCGSHLAVVC
3569	33937	B	3606	1	1830	
3570	33938	B	3607	1	459	
3571	33939	B	3608	30	440	
3572	33940	A	3609	1	279	
3573	33941	A	3610	2	500	

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3574	33942	A	3611	370	464	GHACGAERDHLQPHSPAHLLL LLLSV*AVW*PRYTVKMATAC HQW
3575	33943	B	3612	1	780	
3576	33944	B	3613	1	610	
3577	33945	A	3614	1	1896	
3578	33946	A	3615	2	1418	
3579	33947	A	3616	314	720	GVQEESSDLPTAVDSSRPDIRD QAWASVHWELYVHGSSFINT* GERGAGY/AVITWT/HVVEARS MPQGTSAQKAELIAFIRALELSE ALAKTVRQRCVSCRQHHARQG PAVPPGIQAYGAAPFEDLQVDF TEMPKCG
3580	33948	A	3617	1	1029	
3581	33949	A	3618	1199	1758	KTLSFLSDQPLRARSCLPFSGKI RS/RALAKTVRQRCVSCRQHHA RQGPAVPPGIQAYGAAAFEDLQ VDFTEMPECGGNKYLPVLGRT YSGWVETYPTRAEKAREVTRV LLRDLIPRLELPFRIGSDNGPAF VADLLQKTATVLGITRKLHAAS RPQSSGKGIQNNRTGGVYTPCD IESHVILFRSGY
3582	33950	C	3619	499	831	
3583	33951	A	3620	410	1144	LSIQQYLTRP/PLLGFPPAEDSW FTCLDLKDAFFPIRLAPERQKLF AFQWEDPESGWPPCWRALAAT ALLVQEANKLTLGQKLNIKASR AVVTLMNTKGHHWLTNATLT DYQTLLCENPRITIEVCNTLHPA TLLPVSKSPVKPGCVEVLDSIDS SRPDLWDQPWASVDWELYLD GSS/FLQPPRRGGGYA/VGDTSE LPPCWVCGIPALTQRLEKQHLP PSGHQGSLKHLIWDLLLLTKKR TFSSMI
3584	33952	A	3621	1244	2690	
3585	33953	B	3622	1	1114	
3586	33954	B	3623	1	1863	

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3587	33955	A	3624	3	2056	REALQGIQVRLKHLRTFGIIVPC QSPCNTLLLPFPKPRTKDYSQV QDLRLLHQATLTFHPTVPNPTT LLGLLPAKDSGFTCLDPKDAFF PIRLAPERQKLFAFQWEDPESG VTTQYTWTGLPQGFKNSPTIFG EAWARDLQKFPSRDLGCVLLQ *VDDLLLGHPTAVGCAKGTDA LHRHLEDCGCKVSKKKAQICR QQALAATALRVQEANKLTLEQ NLNIKASRAVVTLMNTKGHHW LTNARLTQYQTWLCENPRITIE VCNSLHPATLLPVSESPVEPRC VEVLDTIDSSRPDLRGQPWASV DWELYVDGSSFFNPQGERGAG CAVITLDTVVEARSLSQATSAQ KAELIAFIRALELS/EGRKGLSPG RGKDK*WRKDGFGYRMGEYC ATAARSCSCTGCARNHPSTSGV TGKVVRPVFLHLAFVS\FAKTV RQRCVTCRQHDARQGPAVLPGI GAYGAAPFEGLQVDFTEMPKC GGNKYVLVLVCTYSGWVEAYP TLTEKAREVTRVLLRDLIPRFRP PLRIGSDKGPAFLAALLQKTAK MGTRSDTQLAHIGTVLRDIHVS VCSDGPNLRTGLNVILGGVEW QSTPGNLVRRQGETGLHLHIYH WWQAVAIFPVYLGSSLHMKVG GRSFEQEEDTEHIPVSYDREGQ ECDTELKGQEGDELEAGSVVP
3588	33956	A	3625	491	964	RIQLCCRTRGTGAQKKRMKVS SRCTPAPATRGTGAWQPQAQQ APGVRATEAPRL*AHDEVSQPA PAPPSTRHSPRR*PVAGKEHLE AAVDKERHEVAQAVVTHVLEG QLEDVAPAHAAQI/GSPPWAGK RLRTNPAPRPCHPIQTLSRRLGP QNHTLLH
3589	33957	A	3626	131	351	NVGLKGTAGER\GGSGPPS*PPA GRNSGPAGRRPPAARAPTPGSA AR*PAPPGPPRPPAGRGAAAAA GPAGGGA
3590	33958	A	3627	3	428	GEWEAPPLLRHTRPGPA/PAPPA PSGASCAPCGGQTCRPRPLRQA PPSPITTGHARIWLGQPRPRSSS ATPPKELP*GPTE\PHTGELWVA SGSCPSGTKLPEEGSGSNTYFSA VSAGDTQSNIIWNGPPANSNRP AAEGPDC

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3591	33959	A	3628	2	425	YLASAAIFRNMSSVVCLVCFFF TSQICLQTDNAPYTVLSINENLS VLGSMFSNFLRSFLRSTKASAK PFIVTLLRSSFFSVSSSLASSSAM HSCSSSNSSSFFNSSRTTSKSSST SSSFTPS/SESF/SS*VSSSRFHSYT PW
3592	33960	A	3629	81	594	LPAGFGPCGAWNQNQREKRPQ SPGAESAA*SGGGQQRGGRAG AGGHGACASLGSE/PQGREPAL GAGGETALPSGSGSGRPPRPQR PRDSGPEALPSAAFWKRRR*AS ASAPALTPVPDSVRGAQPGGG GAEPEGKAVRMRGASRPALSQ LSGREIGPCPQGRVVAPSGTAC
3593	33961	A	3630	317	778	PMVWSCASAARLPEPGNGALL RTSSPRCSP/CPSAA*LTRLPPT/P /PGDPSAAPSPGQRPAGLAGAG GAERSGAVEVGPREPGRDGAG S*SWI/AGPPGRLEAGSA/GVLR SPVAGWRPGTCAGRP/GKAGDL GPSAPPQAPHPPPPSWSPLSPLA SPPTK
3594	33962	B	3631	1	1068	
3595	33963	A	3632	1	730	LALTARSSHPQRATVPKASVVA AASPTKFRHSGAALQWRNLGP VRAQGRRLSTAAPAAPSRRLFP PPPFRGGRGGGWSGSRGRRGA EPGRSHGAGGPGDDGRCGWGE GAGTSTPARPSRGPG*RPEIWTR GGGGSAKSQG/PAGAPGCAGPR GASSFGRQRAPAVLGPG/SSTA VCPLPRRTWNLRAPGGAPSYA QVAAAHQAPPGRPPWSPRGAR GSGRSRTFAPSTPAVVAGAASA VAPPRLRPSPPPAPAPAAAATA AERRGREEAPGRGCGSGRAEPP PLGPDGTQVSPLQRSSRVTEFC GGSGGHYARFWHSSPLRVGAS RSQS
3596	33964	A	3633	70	792	HGLVLDVRGPLSHAAPYWAPY PAATAAAARTAPLPPRSAIV*/S GPQPDFQELRKTWPSQC/GMAR REPLLPITAIPRVVVETTP*GFA KQEPSVAGLRCRGSEAPA*LLH GVHRNVS/ETPGPEMGRPG*GN HRQRPGKQRGIPSSGLPGRCSG SRGPHSSPGQKPHGSTLSGRRG ADPRPRRRVYLSTPLLCEKKPH HDTILKRKPGMGDGNNPCPWN AGLYGQATRFAPLPLCPRRRHG

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3597	33965	A	3634	2	339	WPCGWTGRGGCRQ\RGRERRL GSGVRFGDVSFRGRGRGRARA SWKPPHQGPGEPKSGTRNRPP*\ GGGAPAGIRGPELGTGNMKKL LLSLPIYYHLAGEKGQVAKIVRI PSADV
3598	33966	A	3635	31	438	MVTDVVTRGGELGQRHVPPGE SSGLFCGQCGERETRDPSYRG/ WSRRFRFRALKNGAHWSPRLA VFGDLGADNPKAVPRLRRDTQ QGMYDAVLH/VGNFSNYKARF SMPGDNEGLWYSWDLGPAHIIS FSTEVHFFLH
3599	33967	A	3636	1	422	LRRDTQQGMYDAVLHVGDFA YNLDQDNARVGDRFMRLIEPV AASLPYMTCPGNHEERYNFSN YKARFSMPGDNEGLWYSWDM GPAHIISFSTEVYFFLHYGRHLV QRQFRWLESDLQ/QSQ*EPGSP AVDHHYGAPAHVLTK
3600	33968	A	3640	1	319	FRREPPRGAAAAAALPRRNREN KRSKNRPCCEGPRGSARMKELE *PRPLQVLCLLPEMCSPRLADS YSPVSVRPISAPVRFLHRCCPPP FAEFPACRLLQHSRVPL
3601	33969	C	3641	214	363	
3602	33970	A	3642	1	3390	
3603	33971	A	3643	396	766	ERGLGRSEIPRKEVEHFMQLGS AVAGP*LLP\LVGPAGECFHGW LEPLLARIAEDKTVVVSPDIVTI DLNTFEFAKPVQRGRVHSRGNF DWSLTFGWETLPPHEKQRRKD ETYPIKQPVGVIGD
3604	33972	A	3644	105	786	VGPEHCAGAARWVTSPPRSWP DAGQSVN*PDLP*REKHPEG/G* KLQGQGAKTAGNAVVWKPLS K/PQGSSALSGGHWDRLPAPDP GKMPNCDRAPPKIASRVSPQAC FPRPSPPVPSAGPLRASTPADQA RRPARAARPPDALSKRGPCRIS AKLHSGGGGGGGCREKAQEEP EGRTARSLTPPLPLAPRPGPAGR RLPPAHTTQPPGRTGCPSPAGR DTSQLPYFLLK
3605	33973	A	3645	313	546	RNKVGSRGRAKQLKFSGQSTR VHRSESREEEEEKEEDEEEEEEE EEEYEKEEEKEEEEEEEERDLEF SKGPFLSS*SSQGK/GTRVHRSE SREEEEEKEEDEEEEEEEEEYE KEEEKEEEEEEEERDLEFSKGPF

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3606	33974	A	3646	3	1332	PLGPRRQQSECGAPTLTWPPGS NGLPGQQGASPLSASPGAGAGS GRGPAA\GGSGASCTPSPRGPAS WSRSAAQVPRSSRWRAGSASS* NAGSP/TPPTSQPPRA/PALCAA AGTLAPVEKGVEVPAGRGLSG APS**GKCPLPEAPSGGSAPLS* GGTESGAGAPEPRKATGRPGPR VPGGAGAA/RGLPAPTSGCAAP FPPRPCPGLCVLRARPAGAAHP CPGPGWPG/PGPGAHQTLRAAL REPSPLASPLVSGRPGPRLVFNR VNG/AAGPLHVPILRGDPGDLH SGPRGECPLCVRSLAAGATAA\ DGGPAGEGRPRPVYTMERTAN PRLQNFVPH*PR/PSGGRKQFLA RITS\FPSGCWEGGAATRPTCRQ EKGMAALPTHCAWLGAGHT*K CQHLDFCTFFFPGPGCGDGRCH VQGPNPSDLSPAHCAQGPATSP WGWQGGAPG
3607	33975	A	3647	102	788	GHCGGGTQCSWPAPWCQNLLP PSASPTLSTQRQLWHAWPGAH RNPV*QVPSLDS*ARAQLSVPA QGSLPLC/ASLTASPWCSCSSLA VLLFGK*PFCVNLF*RASLMKS SSRARVLPSLRPVRWPAVG\RG WQGMERGQGAWPWLCGAVCS RA*SVHMTTLPSGPALCGIQRR LQSSTQRRPESLHPLQLGWEAA QAGEGLPHPAVVHLPASPRLQL SQLHQSRPRLPPG
3608	33976	A	3648	114	1309	TNCSCLRDRPLDSSHVPWVEEA QSAHNNKEIVPQKGPWSSKHN QARGPPRSESNTNKAVNCAGRS TKTQTPRGTSGT/TEGNT*VHTR HTKMSTTNTNTSSLDAPPTTQQ MRSTRERGTS\PAPPSSALKNTY TLPLPTS\SNDTTIYQLTVVPGP GPRTGELPRCHARVTPRVSGEE ALPPPPRSPENSNTHLRTPSQTR TPTRARPPL\PETSPQQPWPDPR VGFFLRSSPVWAPSSQQYPWW SPSLSTNMTIPPESS/SLLPTLAY YTSLTSHHGQRMPA/PADHA*A QSTPSAHRHRPQYVQWTTDPPS THGTFEESSGR/YPQTHTVAVK KKTIGTPARDSHSFPTTPTTRM VKSLKTSTGTSTDLSSSRSILKS PTSSIFTSLTIFSIWRDPDSMDLC V

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3609	33977	A	3649	3	1777	NVAGNPARSMAETQSRAGTAG PGPRTKQTPGTWGSGQAGAPA HPPCYIQESRSGFSAPGRARNA\ PGAANPLCMAPGGAEGSGVIQ REVEGRPRSHSAPMLSLWSERP PSCVCLGPDGAADFPRRGRGPR PPLQDSPASPSAPRCSPARCSRL PL*PRPRDKDAPGTGGRPG/PPG TLPDSRLECSASRPCGEGCETL VQFPDRRGPGCGPLQGPGRGNP ARPQPRLTRAAP\GPTAPAALVS SGGAAVPPRRTR*PLLAGAVEV ASPRPGSVQSLVPEHPGPFKELR NIVLSNSPEASYSAPAN*RPPPA EIRRREWQELRGGVLGGGLVFS FPPHSCVGSTGAWGLPTWRGV GSGIQGFFSVPP/SGRETSRGGR TATAPWSSTPDCPSHWREPSAG SLRRG*GRRDAAPGAR*SRAPP TRPGSRASPG\GAGEAGVEGEL LGPRGQVVTG/PGRPTAPGIYRP GGRRKASAAGSRCATGGSRSSC PRRGSRSPGWRWTRWGVP/GR RGTLARPAPGPGCPYRRRPGGA PRGAGGRPSTGCGSRSRQWLA GQLLPRPSMLGALPGLAPLQPP PAPPVPPPPPPPPPMPLSAALSS
3610	33978	A	3650	3	922	NVAGNPARSMAETQSRAGTAG PGPRTKQTPGTWGSGQAGAPA HPPCYIQESRSGFSAPG\PRETHS GAANPLCMAPGGAEGSGVIQR E\GKAGPDPTARLCSAFGPSGRP PAC/RLGPDGAADFPRRGRGPR PPLQDSPASPSAPRCSPARCSRL PL*PRPRDKDAPGTGGRPGRLG HSLTRAWSAQHPGP/AGEGCET LVQFPDRRGPGCGPLQGPGRGN PARPQPRLTRAAPAPDSAGSSG/ APPEGCCAPAKDEMTPAGRSC GGCLAETRICPVARP*APLEKSF PNVVNPGKKKAQPTLSPSNMT
3611	33979	A	3651	1	542	LPGAGHRRVLDAGGPRGAGLQ PQLPARQVGAVAELHVSGPPG AGLA/GSGSGASGVGLGAAGW GSGPRGVRAEGEGAYSGPGQV FPVQGNVGNADAGTTGVGVPA GWWPPLPTRLQTLSVASPWLCP *AAASARSPPSGLSGE*TLFYTF SFLPPVVIAASPPAGLASEARPC FPRFHSYP

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3612	33980	A	3652	1	3063	MSLEVDRSVETMCSGDEILLPD LPKADVADPLWGPFPVQNCLS LARSDSREQGLVLVMESRNRE VVPPGVSYSKDGAKSLKGDVP ASEVTSKDSTFSQFSPISSAEEC GDDEKIKVDDPLTRRTCNQASG SAPQQDYDKLKAFGGENSSKT GLSPSGNMEKNKVVKREAEAN SINLSVYEPFKVRKAEDKLKEN SDNVLENRVLDGKLSSEKNDT CLPGTAPSKTKSSSKLSSCSSAI MALSAKKAASDSCKEPV
3613	33981	A	3653	1	847	MENKKVASPGWTCWECDRLF MQRDVYISHMRNEHGKQMKK HPCRQCDKSFSLSHSLCWHNRI KHKGIRQGPDSRRTFTKRLMLE KHVQLMHGIKDPDLKE/TDRCH P*GGNRNKRRQPRSPVPSRSWK NQFWSSGLPKEQSLNH*KS*KS MFLRFTSALVRGFTTENLLQFH EHIPQHKSDGSSYQCRECGLCY TSHVSLYMHLFIVHKLKEPQTV FKQNGAGEDNQQENKPSHEDD SPDGTVSDRKCKVCAKTFETEA ASNTHMRIHGMAFIKSKRMSSA EK

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3614	33982	A	3654	854	3009	VNSHSQLLQRE*NT*ESNLQGM *RTSSRRTTNHCSMK*KRIQTN GRTFHAHG*E/RVNIVKMAILPK KIQSDLTSHEISLEEMKKHNQG KEAAQRVLSQIDVAQKKLQDV SMKFRLFQKPANFEQRLQESK MILDEVKMHLPALETKSVEQE VVQSQLNHCVNLYKSLSEVKS EVEMVIKTGRQIVQKKQTENPK ELDERVTALKLHYNELGAKVT ERKQQLEKCLKLSRKMRKEMN VLTEWLAATDMELTKRSAVEG MPSNLDSEVAWGKATQKEIEK QKVHLKSITEVGEALKTVLGKK ETLVEDKLSLLNSNWIAVTSRA EEWLNLLLEYQKHMETFDQNV DHITKWIIQADTLLDESEKKKP QQKEDVLKRLKAELNDIRPKV DSTRDQAANLMANRGDHCRK LVEPQISELNHRFAAISHRIKTG KKPSWRRGVSNLGEMLVEVYL KALMSEDLRKGINQDEFSPTIY YFPITVFGSEGDLLLGKIRWIQG AYCLMIGQDVFMDTRLRVSAC FLKTKMKTVLVVFDQNEDNEG TVKELLQRGDNLQQRITDERKR EEIKIKQQLLQTKHNALKDLRS QRRKKALEISHQWYQYKRQAD DLLKCLDDIEKKLASLPEPRDE RKIKEIDRELQKKKEELNAVRR QAEGLSEDGAAMAVEPTQIQLS KRWREIESKFAQFRRLNFAQIV
3615	33983	A	3655	44	953	GVHNGVEELILVRRMQKSPGP GEMESGSLEKEPLGTQTGPVPS E/EYGIGLSQSISTKHPETSPKDS RIRENDVTADGRTTEDHITADP GTTEDSVTADPGTTEDNVTVDP GTTEGSVTADPATTKDYVSADP GTTKDSVTADPGTTENFVTADP GTTKDSITADPRTTENFVTADP GTTKHSITVDPGTTEDSVTADP GTTKHSITADPGTTEDSVTADP GTTEDETTKHGDTHLL*TTSVT AVKPTRLLTPMGIILISLAATTV TVVLFVGLGFIVKECFLPPLNPS TRVIYHPHVMDYSTP
3616	33984	A	3656	200	542	CSPPSTRPGPGP/SGTAWPGPRG TKRSSPSSSSSSPSTTSTTTSSSSS SSSSSSSSAPPRGFSSTRPSPLRR LLPPSSSSPSSSSSSPSTTSTTTSS SSSSSSASAGGRRAGTRG

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3617	33985	A	3657	132	853	EIDKKHRFLVSISLNSPSK*GEG DTPSRPHRARTGASVVPSPKFPT SLGRSALSRHPHQTTNPTRPLR KAGAAAFNAPRAGPLGTAWPG PRGTKRSSPSSSSSSPSTTSTTTS SSSSSSSSSSSSAPPRGFSSTRPSP LRRLLPPSSSSSSSPRSSSTGDEA AAAAPVA/SRGAGPGA/SAAAA AAAASSSPG/SGAGAGPGTGGG SPGRAASLAGAGAGPAGCSAA PPRRLPRLERLARRRAC
3618	33986	A	3658	222	373	
3619	33987	A	3659	3	513	IPAALSCCCPEWQALV*QILQDS SCCQSPRVPGHSCGKGTTLCVF SREWSLVSGSRC\SDGETSCTGR CCNAFLCYDLRFSWLFCTLDVR RGVA/GQGGRLGLDLGLSAVCI HQVWVMGSRCG*QLLAPGRVS RPRGRERGTHWSCWCRSPWM GSGWEAHSGAACLSGVFVP
3620	33988	A	3660	3	463	
3621	33989	A	3661	263	1020	SGLREPKQLQMLEL*RKMSQLS LEG**SSHNM/V*RL*KKCSDYS YRDYILSWYGNLSRDEGRTLPS ALGR\FWEIARQLHDRLSHVDV VRSCLQGCCEDLYSLISVT*KLP MPDMKNSQDLLCCT/PCLRNSD DEVRFLQTCSRVLVFCLLPSKD VQSLSLRIMLAEILTTKVLKPVV ELLSNPDYINQMLLAQLAYREQ MNEHHKRAYTYGPSYEDFIKLI NSNSDVEFLKQLRSVEGTVEKS GRRCVLVVFNN
3622	33990	A	3662	1	4314	
3623	33991	A	3663	2	492	ISAGVTGTSGLSAEATGIPGLSA GVTGKTGLSAGVTETIGLSAGL SARVTESTGLSAGVTGTIE*SAV VTETTRLSSGVTGTIGPSAEETG ATGLSAEVTGTTGSLAEVTGTT GLSAGVTGTIGSSAAGLSS/AP*I PSIPAFSGLVFILSCSTKFKAKE WLFFV

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3624	33992	A	3664	1	959	AGLSLMGSI*ACHTGLESSLPV WILSAPSFPPHPVTSSPPISFHLC/ KLSLSH/CT*LGTVGALLPASSA THVHQAWPQWPATLMSHWNC YPREGEEIGYLPTSHPTPHYIPV LTTSA/HSAAPSHFGQSQAPIRL PPPPGAPSISLSPLPQNLCKGYE RDPLPSRPPLRAVRSKKQKLGW RLAGPLSKSPDGINLPFLTSPLG CLDLSLPPGPGPTVLFSVSLWH STKLCQHQSLTGLGGQPGQQG SSSPSAVFRGSRDVSGVIAQRQT SQEKELESGL/CVLTSGAPSPSSP HPPYRGTSLFLFYLCILEKGKM VNKRDLCC
3625	33993	A	3665	2	2180	CPQSLIAVEQRKPPPTGSQVLLQ PRAAQGTPLPTATPHGTSGDAQ KHLLQTW*NTWP*KKPGPSPT/ VRRTQDTDQTTAQHPEGAKVQ GHDQFPGGSVHFGCRPAPSPPR RQG/PLAWHGAGADGFPH/GSP FPSSLTRRCTATPSVLKTSPYRK PLLHSCPSN*MYP*PTRPPPSPTS PTQLSLRT/ANVATCPPLWPLPL RRHLSQWVPPNWEPGAASGSS REHGGI\PAMPQPQCSAPSY/PPT EACLQSADGDQALSKHSADTN AS\RPKPRGSWCPPVTDEDAES DRGSGQQQSQRTPAEVLGKPQ VLERFLLPTQTKQEGSHDEETR HVHNCREGSTEKQGRHPLPARP SPASSKRLL/TPGPSPPAAKRLL RQGLLRPAATPCSASGGYLGTR QRALGAGALGGCEPTPATGEES RPCHLR*PLSPSDSSSLCPLGFA K/PHQARNAGLLGASTGMKAT KWAGACRQRTAKTEAWASSW QRVSDTKP/GSTRQKNKDSGSH PQYQAFDLRLTITAGFSAAEAS ELEGSCAAATQISSLQVACHGT SRPHNHVVDDIMNSTAGPPSGV CGELENVMSGKPTQLVSEMLQ VR\PSPSGASFQQSLRMT*VSVN WTPPRPCI*NRP\AAPAETSPAPR TA/STPNASPQGPSARGFVEKW NGSHAARHPRYKPGTQ*PSGA ASTG/SPGTPPSPALPPCRASSLV
3626	33994	A	3666	3	426	
3627	33995	A	3667	3	266	

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3628	33996	A	3668	2	1256	CHCGPP/VKVEAYGSQVLKGVL AQVQLTVGPVGPRTHPVVIFPV PECIIGIDMLSSRQNPHTGSLTG RVWTIMVRKAKWKPLELPLPR KIVNQKQYHIPEGIVEISATIKD LKDAGVVIPTTSPFNSPIWPVQK TDGSWRMTVGYCKLNQVVTPI AAAVPDVVSLLEQINTPPGTWY AAIDLANDFFPIPVHKAHQKQF AFRWQGRQYTFTVLPQGRWEI NMTKIQGPSTSVKFLGVQWCG ACQDIPSKVKDKLLHLVPPTTK K/EAQCLSGFRREHIPHL\PIYRV SRKAANFEWSPEQEKALQQVQ AAVQAAWPLGPYDPADPMVLE VSVADRDADWSCWQASI/GHK VGHAQQHSIIKWKWYIRDWAR ADPEGTTKGQGQRRWWQLAE RQDSRDREAAIGERQETAVGKT ARDGEAVCD
3629	33997	A	3669	349	718	AGPEGTTTAECP/I/CQQQRPILS LRYGTISWG/DQSATWWQVDY IRTLLSWKWQSASAKTTIHGLT KCLIHHDIPHSIASD*GTCFMAK EVWQWYCFSHSQDSRVQESRG GIGSCTTHHHPCSFPN
3630	33998	A	3670	667	960	
3631	33999	A	3671	1	1371	
3632	34000	A	3672	1	942	MVGKAKWKPLELPLPRKIVNQ KQHHIPEGIAEIAATIKDLKDAG VVIPTTSPFNSPIWPVQKTDGS WRMTVDYCKLNQVVTPIAAAV PDVVSFLEEINTSLGTWYAAID LANAFFSIPVHKVHQKPFAFSW QG/QQYTFTVLPQDYINSLAL*H NLIWRDLDYF\LLLQDITLVHYI DDIMLIGSNDHKVGGAQQHSII KWKLYIHDQAQTGPEGTTTSVI AQWAHEQSGPGSRDGGYAWA QQHGLPLTKADLATTTAECPVC QQQRPTLSPRYGTIPSLPLTKAL TLQLKKCSSGPMLMEFTGLAM FPIILKQLD

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3633	34001	A	3673	1	1270	MGDPSRRRTCRAMQAKYPLVF KGCGVCWGSLDPRCRVASQV WPIPKRLSRGWPFHNAVGRQV SDWKSGQDFADFGTTHQTGFS PAGANQRGPLAATLSGPGGEG QSAVARLTGEKKNHPGAQYAN RLSPRVGRFINAAGTTGFPTGK RAVSATQLMILCLLPGYLCNGK RKLSAIQGLLDNGSELSLFPENP KRHCGLPVKVGAYGGQKTDRS WRKTVDYCKLNQVVAPIVAAV PDV/VVSLLEQINTSPGTWYAAI DLTNAFFSIPVHKAHQKQFAFS WQGQQYTFTVLPQGRWEINMT KIQGPSTSVKFLGVQWCGACQ DIPSKVKDKLLHLVPPTTKKEA QHLTGLFGFRRKYIPYLGVLLC PIYQVTRKAASFQWRPEQEKAL QQVQAAMQAALPLGPYDPAGP MVLEIAVADTEAVWGH
3634	34002	A	3674	1	1978	LTIYAVNLSLILPQGDLWPFTRV TVH*GKGNDQTFQELLDTGSEL TLIPGYPKRHCCPPVKVRVYGG QVINGVLAQV*LTVGPVGPRTH PVVISPVPECIIIILSSWQNPHIGF LTGRARAIMVGKAKWKPLELT LPRKIVNKKQYHILGGTVEISAT IKDLKDTEAVTPTTSPFNSPIWP VQKTDGSWRMTVDYCKLNQV VTPIAAAVPDVVSLLEQINTSPG TWFEWSPK\KALQQVQAAVQA ALPFGPYDPADPMVLEVSVAD RDAIWSLWNAAIGESQRRPLGF WSKALLSSADNYSPFERQLLAS YWALVETERLTVGHQVTLRPE LPIMNWVLSDPSSHKVSGAQQ RSIIKLKWYIHDWVRAGPEGTS KLHEEVAQMPMVSTPATLPSLS QPALMASGGVPYYQLTEEEKT RAWFTDGSARYAGTTQKWTA AALQPFSRTPLKDSCEGKSPHH PVIAQWAHEQSGHGGRDGGYL WAQQHGFPLTKADLAMATAE CPICQQQRPTLSPRYGTIPQGDQ PATWWQVDYMGPLPSWKGQR FVLTGIDTYCGYGSAYSARNAS AKTTIHGLTECLFHCLGIPHSIA SDRGTHFMDKEAPSASVLGLA LALLAPQLADSLLEDPVIVKGT DEAEYFQSVREEPDSGVKRKK MLKSGKNY

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3635	34003	A	3675	1	746	MGKIVQPEKAVSAKAGVCLKG CDCSEYKVQCEWQDTSPKYLG IVLSFGEEPVTHLRWDLHAWSY ALSKVISTICRRGKFSEFKAHTA PVRSVDFSADGQFLATASEDKS IKVWSMYRQRFLYSLYRHTHW VRCA\KFSPDGRLIVSCSEDKTI KIWDTTNKQCVNNFSDSVGFA NFVDL*PPSGTMP*PSAGS\DQT VKVWDVRVNKLPTALPRMVY YGAKCHLWGCWSFTENSELSF QLFCTSIPIWF
3636	34004	A	3676	5	812	AAGSAGLPATPQPRARRVGRR RLGPGARGAGGAGGAAGCRAL RATARAAGSQPGPHSPGRTARS ARK*RLRRPESNKVRVCGPHSP APRTPPSSPGIQHAGKPRARRPL PPPGAGVGLGIVPGLGLGRAGA DVAGRVGPGAGVPGCCREGAR RPGSGRRAAPVLSPLC\PGLQTA RAAAGPAPGA/GWP*VRRLEPA EALPSGMFMMRKSCSVALTSSL SSSPSSSSSSSSSSSPSLTRPDVS PRVTAATGDMYRGSFSGLTKA LRTWPR
3637	34005	B	3677	1	1071	
3638	34006	A	3678	1	169	
3639	34007	A	3679	2	189	
3640	34008	A	3680	3	352	SKHNLKLTATSQPHRPMQLKP ACVPPVLSSPHMWGRSDTSEGP AH*PPA\AWRVCVVLGL*ASPP AKLQAQHQAGSTRPVDRQAPS VLTAPPLVWPPFPQGICSKWGA QHGKRGQGH
3641	34009	A	3681	8585	9026	ERYKFFSAASPNILILLTFFKIVV RPLITKENLYLEILIRHSLLCSVL TLVCVFCCPVFIGSCSSKRLTTA WTHSTGLCAAMSSPRPGGGGG KGGPAPWAGKRAGSGG*GEGR GKERVCGVQAPSVPTGVGMGG QRRAGVGGPRAAP
3642	34010	A	3682	2	484	
3643	34011	A	3683	1499	1793	IHSIESSPIPHWIGGLRLMLCIVT RLNFEICLVKHFIKQCKVVEHT QQYEWHRVLHLKKK*QALNLK KNLQT\GDKKL*VSSLVHGETN SCRSKALAL
3644	34012	C	3684	1	1044	

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3645	34013	A	3685	8504	8970	ERYKFFSAASPNILILLTFFKIVV RPLITKENLYLEILIRHSLLCSVL TLVCVFCCPVFIGSCSSKRLTTA WTHSTGLCAAMSSPRPGGGGG KGGPAPWAGKRAGSGG*GEGR GKERVCGVQAPSVPTGVGMGG QRRAGGGEGKGALARRLGGG
3646	34014	B	3686	1	2178	
3647	34015	A	3687	1	2424	MLTVIHSEMQAAKVSDGNEELI GKWNLLGIERPWGPRRDWSGL HGPGPGTPTARPRPLRDSSQNT WRLQLKPRLKGGPGAQNARM NEAWQPLPRFQRIYEKTWVPW QKHDAGAEPSQRTSTRAVPRGS MELEPPHRAPRAVRRVPQFSRF QNGRSTSILHPVPGKAAGTQLK PVRADLVAALYKATGAELPKA LGAHPLHQCPLDVTDELLEKIA SRSQNIIEINISDCRSMSDNGVC VLAFKCPGLLRYTAYRCKQLS DTSIIAVASHCPLLQKVHVGNQ DKLTDEGLKQDNQPQCIEGNFE SRMHAQGRTLVQERPKKTVNFI TVCLLGPVQAGSKGQGRVVNG KVLTSTANLRRISVDGKSEKSV KDAEKAFDKIQQPFMLKILNEL GIDGMYLKIVRAIYDKPIANIIL NEQKLPWVVDGTGRCGAGGS VTGEARAMQ\GPQWGKGRLRH GGLQVPIPALQGGS*GPARN*A QQLLAQRIKYL*IQLTRDVKDL FKEN*KPLLKEIKENTKKWKNI PCLWI*RINIVKIAIL/PKVIYRFS AITIKLPLTFFTKLEKKTTLNFI WNQKRACIAKTILGKKNKDGG IMLPDFKQYYKPTVTKRAWYW YQNRYIDQWNRTETSEITPHIY NHLIFDKPDKSKQWGKDSLLN KWCWENWPAIYRKLRLDPFLT PYTKINSRWIKDLNVRCTTVKI

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3648	34016	A	3688	453	1508	KAPQAPNINSYCLQVEECCQKG ISVDLSTGMTSTGVVP/HYNEQ VAGEKEEETNSVATLSYSSVDE TQVRSLYVSCKSSGKFISSVHSR ESQHSRSQRVTVLQTNPNPVFE SPNLAAVEICRDASRETYLVPSS CKSICKNYNDLQIAGGQVMAIN SVTTDFPSESSFEYGPLLKSSEIP LPMEDSISTQPSDFPQKPIQRYS SYWRITSIKEKSSLQMQNPISNA VLNEYLEQKVVELYKQYIMDT VFHDSSPTQILASELIMTSVDQI SLQVSREKNLETSKARDIVFSRL LQLMSTEITEISTPSLHISQYSNV NP*RGCFHYCLAFT*T*SNTLSI YSENVQEGLVKGN
3649	34017	C	3689	57	230	
3650	34018	A	3690	2	123	WWKV*KKYSGFKVFL*HQH** PRRPLQSLFS*MPWKRIAK
3651	34019	A	3691	94	360	LMSLLTSPHQPPPPPPASASPSA VPNGPQSPKQQKEPLSHRFNEF MTSKPKI\HCFRSLKRGVSSAPE SCLSGVLWLHVWFCITNFVCE
3652	34020	A	3692	1	2037	
3653	34021	A	3693	2	1079	NLSKKYQPKKNSKEEEEYKYTS CKAFISNLNEMNDYAGQHEVIS ENMASQIIVDLARYVQELKQER KSENDHRVSGASRRAPLPGPFR RLRPFTPDVGGEEAAANQAE\Q *YPSLKWNSKGKTNGTRNGTK CGKEHSPTLHQSRQGTVIQSAN RPSVA*SYRAPLHPSPH*KLAP* VPAFSSSRVFPMLSSFSL/YISTD DQEGLYSLYFHKCLGKELPSDK FTFSLDDSQLVIEAYKSGFEPPG DIEFEDYTQPMKRTVSDNSLSN SRGEGKPDLKFGGKSKGKLWP FIKKNKSPKQQKEPLSHRFNEF MTSKPKIHCFRSLKRGIQPPDG NEKQDDTMASSFTFSLSLDYEM PVIEKAE
3654	34022	A	3694	1	215	MAQDYGAMGDLVLLGLGLGL ALAVIVLAVVLSRHQAP/C*PPA FAHAAVAAHSKVFSNIVRERV KTQEAERA
3655	34023	A	3695	1	208	MAQDYGAMGDLVLLGLGLGA\ ALAVIVLAVGLSRHQAP/C*PPA FAHAAVAADSKVCSDIGQRTC RDATPT

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3656	34024	A	3696	1	164	MRYRYIPVRMAEVRT/SDETKC W*ECGATGTFIHCWLANIQQHT LSRLFTCLCSC
3657	34025	A	3697	146	659	LAGPRCTTSLTPSEGG/LPPPDSL GYTVHPPDSQGHTGPLPAREGT GSHRFGVE/VRQRRWERGEAPL LQLSPPAGRPPRRPHPCRPQHLP SAAISEAATARGPRNRSQAAAA AADPDNLRVARG/PRSTRSSAV DAGPPP\SASPGFP*SSSQQRPSP EKTGSEVYSAYIPANC
3658	34026	A	3698	32	376	
3659	34027	A	3699	1	2148	MALSPWTPGLGAGEKLVQAAA VSTGPSLELCTLPSTLGSSVAVE ALEQLFVVECVRDARRLNLFEI NTIKMRITRTENEIELLKKKITD LTKYNEALGEKQEELARKHAR FVLSLNQTMEKKATTTVYINET YTKINLKREDIALQKKCIQEAEE LMEKERAEYLIRKQELTAQINE FENTREVKRMETYQKK/QRIG*I TN*NVKNKRNSY\FSAAVLSDH NLEIARLHESIRYWEQEVSELK KDLAILEAKLCFFTDNKEKLDD ISNDEKNEFLNKIKQLVETLHA ARMEYKDLREKMKTLARQYKI VLSEEEKAFLQKQKIHDENQKQ LTFISQKEYFLSQKRVDIKNME EGLITLQELQQVILSFMSSVYSK PNLSHSRGLTCCSFPLYLQMMT PFPCVITQWKMACLRKKHARW TAKIKAEIQAITEKIQNAEVRRI ELLNETSFRQQEISGFVAQIEKL TTELKEEEKAFVNKEKMLMKE LSKYEEIFVKETQINKEKEEELV EYLPQLQVAEQEYKEKRRKLE ELSNIITEIIWGFLFEQEDVKQEL QQLRDQESKKNKDHFETLKNL ENGFYINDQKADLLLLENKKLK EYILYLKNNIEKYREGQEALMH TSSDLSRQLIAQEGLLQVEEQGI QWWIRQSPKASQVGKPTVQPS VCGQRPKSPCQTTGVNPRVQK LKNLESNVRGQEASSTGERGIL

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3660	34028	A	3700	1	2658	MQAPYRCQRTGWLQQKRLKA GLWGLESSSWSLGPLGQAAQQ ELTSAPGQFRLPPPPQAPERPTA GGSASLGPPLP/PGKLSEVPEPS RPGRPRRPPSTWAPPGGP/GASA LPVVPG/HRGARTRGASTRGAS/ EAGPHLPIPVTSNAPGHAGGW\ GAPSHQNHASPCTGRGPQPAGE LRQA/GEQFPNSWGRRGSCRTC SVVLGHTEPRPEPAHVLVR\GN PGSPVGAAWGNEA/GHPRAPG AQRGG*RSPGLRE
3661	34029	A	3701	31	556	
3662	34030	A	3702	3	1394	RKKELQHKIDEMEEKEQELQA KIEALQADNDFTNERLTALQEN QTRAKESDFSDTLSPSKEKSSD DTTDAQMDEQDLNEPLAKVSL LKDDLQGAQSEIEAKQEIQHLR KELIEAQELARTSKQKCFELQA LLEEERKAYRNQVEESTKQIQV LQA\QWQRFHIDTENLREQKD\ NEIASARDELHSARDEMWLVH QAAAKVASERDTDIASLQEELK KVRAELERWRKAASEYEKEVT SLQNSFQLRCQQCEDQQREEAS RLQGELEKLRKEWNALETECH SLKRENVLLSSELQRQEKELHN SQKQSLELTSDLSILQMSRKELE NQVGSLKEQHLRDSADLKTLLS KAENQAKDVQKEYEKTQTVLS ELKLKFEMTEQEKQSITDELKQ CKNNLKLLREKGNNPSILQPVP ARIHRPIPGFPDMVIRSIVERKK PWPWMPMLAALVQVTAIVLY VPGLARASP

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3663	34031	A	3703	1	1133	LEEKEQELQAKIEALQADNDFT NERLTALQEHLLSKSGGDCTFI HQFIECQKKLIVEGHLTKAVEE TKLSKENQTRAKESDFS\DAVSP GKD*GSDDSTDAQMDEHDLNE PLVKVSLLKALLEDYRGGYRN QVEESTKHIQVLQAQLHRLHID TENLREEKDSEITSTRDELLNAR DEILALHQAAAKVASERDTDIA SLQEELKKVRAELERWRKAAS EYEKEITSLQNSFQLRCQQCED QQREEATRLQGDHTDEAADLP LSRHSVSDPGVSCTQEEIQEAR GLTLLCFSKIKCSQKQSLELTSD LSILQMSRKELENQVGSLKEQH LRDSADLKTLLSKAENQAKDV QKEVKRKDIMSPIMVGLKAKS
3664	34032	A	3704	1	540	
3665	34033	A	3705	1	280	
3666	34034	A	3706	2	416	
3667	34035	A	3707	309	908	LPSRGAGLGTCRPPCLSLPLLP WAPVLPEPPRRVPPPAPRRPVG STTQGLRSASTRR/VDWQAAPP AALVWDPLGEASWAP/GVWCA AIDLANAFFSIPVHKACQKQFA FSGQGQQYTFTVIPQRYISFPAL CHNLI/RRDIDCFSLLVVHFAWK EKWSDVRLGTDSWAAASGLA GWSGTWKKHDWKTSPLVIHEQ KFCFLFP
3668	34036	A	3708	1	2973	
3669	34037	B	3709	1	1053	
3670	34038	A	3710	1	1178	
3671	34039	A	3711	3	247	DCLRVLWCPPV*F/QRSPSLQQP L/RPGFEPLVGRHLMRPARSWR PQPSSASAGLPSSPFRDGCHRFR ASWALGGRAAEGEVAI

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3672	34040	A	3712	137	2176	LKNPPQTHPRRGHLLLISVWGH ILRACGAWQEAKPKAKWPQIP EEKEEGQAPRACTLPGCWRLL RRGQEEKEENWVPPACTLSGC WRLEAVRQQQREGDGDFGAAS CSDLAFRCASSQNPRSLEPVASS PERRRRQPSRAPLGWALKEPGS ERSPPLLSCVEALQPPFLLGLGS GAFCLTRGEKGSPDQDPFCLHS PWMLEAGGSDAATARGDFGA ASYSDLAFRCASSQSPRSPEPVA SISERRRRQPSRGFQILRSSGAFL LDREHVCLASSASTTGLGSPRP SWSHQVASNKGLKPGLRGCWS DGERGTTLEDTRVLLSNPLLLR KGGRKVSTSRLMQLCSVVEKY CPWFLDQGTMNIEIWEKVARA LKKAYRDGAEDIPINIWSVWAL VHPTLEPFHTDHDEEESEEEGE YNEVTKEVTEQFCLPAKAAKE GGNPSLTSPQQLTTETEAEIQLI EKQVHKAQINRIDPEKTLDLLIF PTQHSPTGGVVQEQDLVEWLF LPHSNSWTLTPYLDQIATLIGN GRTQIVKLHGYDPGKIIVPLTK AQIQQAFINTLNWQTHLADFM GVLHNHFPKTKLFQFLKLTNWI LPRITKFKPIECSENVFTGRSSN GKASYSRSKNKVFQTSYTSAQ KAELVAVIEVLTAFEMPVNVIS DSAYMAHSTQLIE/TAQL*FHTD
3673	34041	C	3713	1	784	
3674	34042	A	3714	87	447	AVQRRSGVGPACLSCGSANPGP PPGTSPGAGAAPGGGRWARAK SGPESPPGT/GPPQPA*APQ/AAG PKTRAGVSFLSPPLASSPGHANF GPDSFLGDGVMRQA*RSENKQ DPA\GTPGTWVR

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3675	34043	A	3715	3	1435	RGPSGPRTVSPSPAGASSVGGPP VQAWPCSLCVGSLEPRGSIGGP PKGLQLWGPRASWFLGDYACP LLASAPVLAACKTLCQTPAVPA SL\G*RPLVAVKTHVAAQPFLRI KHLAAVLADKSAPGLRPVCGT A/GFAGYLCLPHSLPSPDG\EPV DVSTLDSAEYCQLGLGGICRGP GR*EGGHGY/RGSEKPHSTYPSS PSLSG/EPENRG/DPGVAQEP*P PPREQAGPFSPFVILEAAPFSAG ACFPGSEAPGGSSPPN\GSAVGL WRGRCPPGPRSL*RIAAAWPEK RCLDSWKG/RRDGAARGVGTA ATFSPPFASRLVLPGEASLGTPG VVFLLRAGEPSASGFPGPAWRE STAGASGGGCCGHGPCSGLRA AGLPSGAGSW/RGDCCHLGMG EDPLG/PW*SSGTPASARGSQEV PAT*GRAGGRAARHPQGARLPS GPPG/EPGSPGFWHRKESQSTLT FLGAQGSSSPLADLGSLGASAG
3676	34044	A	3716	1	756	MNDAGNHHSHQTNTRTGNQTP HALIHKRKLINENTWTQEGEHH TLEPFGGTTDRIVSPSHTRSPDM AIANFQSSGCSVVPDTIPRPQYQ CRSRHSVLLTSNLTVPMQSCVK PPYMLLVGNIKIWMNNQTVRCI NCHVYTCITSHFDSRKSVMLVL AREGIWILVTLPRPWESSLSIRLI NEVLQRILKRSKRFVFTLIAVIM GLITVTALATTAGMALHQSVQ TAHFANDWQANSNQMWNSQQ GIDQ*EHMDTGRGTSHTGAFW WNNRQNSFPFPYSQSRHGNSQF PKFWVFCCPRYHPSPSV\QCRSR HSVLLTSNLTVPMQSCVKPPY MLLVGNIKIWMNNQTVRCINC HVYTCITSHFDSRKSVMLVLAR EGIWILVTLPRPWESSLSIRLINE VLQRILKRSKRFVFTLIAVIMGL ITVTALATTAGMALHQSVQTA HFANDWQANSNQMWNSQQGI DQILAAI
3677	34045	A	3717	3	131	

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3678	34046	A	3718	2	424	CGRKSRGTALPTGSSPQSGPAA PGHSAASALHPTP/SPPPHPL\PP AATGDIDGNRYPATPMTKYPS ASARRPVHRPTCSGGGSHTNHA ESLPPLTPLEEADTHPPGGSQ*T RPPHCIRTGSCLPPPREAPYTRR ERRRHPP
3679	34047	A	3719	1	418	
3680	34048	B	3720	361	1371	
3681	34049	A	3721	1	469	PGTCRGSTGQP*EACWRSP*SV RNTRCPVREEPASPGWSSCLTS PSARGWWACS*RLPSSSCPGST AGSSSGTLCREAAPCHR*AACS DGKPPGMPRSTRRLGPSGARSG SARRCPCGDGPESLRGHAPARA ATQAPDPSTQSSASSATPRAPPL L
3682	34050	A	3722	117	871	GPQSSAGNAGPQRRRTTLGVPR TWHPGPAA*AGNSCHISFYSSR FQPFLGVTSVLRGSSVSVSGIPD HLGQPRSSQEPSRPENAAAQM* TGCPGYAGCTVA*MKGRAELQ GLRTIAAQPGQWLTLLPRCPST RRLGPSGARSGSARRCPCGDGP ESLRGHAPARAATQAPDPSTQS SASSATPRAPPLLGLCGGGC*G DRRSQQGTE*A/VAVPGMLGGP SPFSQPEHPSAFAQPSSCLPLGL DFKLLIPSQ
3683	34051	A	3723	110	1017	EAANEPKHLHQLRHAGLGQHR QAPRPQGRPFARPHQGQDQTD RLHHLQGGGRHGARGHLHQA GAGQSAPAPKGAHVQGPCGCH ESTGPVEH*SHGERPKHRCPRP AL*EHGHENPHK*SSPHDQR*Q TADPEGDN*SQCCPTAN*IPLRK LWLRG*DLCGRSHGQQ*PHQG W/HLDAQLLTPASSSTLCPTPLQ QPLHQLRHAALAQHRQSPPAA RT\PLARPHQGQDQPDRLHHLR GGGRHGARGHLHQAGAGESAP APKGAHVQLVSKQLGGVAAEA HVDSSGLWVSPGPRHN*YKSKS SRL

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3684	34052	A	3724	3	1092	LVEPGRLLEAQGFDKNKR*RRR GRVCGRGGEAPAPGQGQGQPD *NKGKEEV*NSSE\EESSEVSLP KTSREQEIPSLACEFKGDHLKV VTDSQLQDDASGQNESEMFDV PLTSLTISNEESLTCNTEPPKEG GEARPCVGDSASTPKVHPGDN VGTKVETPKNFTEVEENMSVQ GGLSESAPQSNFSYTQPAMENI QVRETQNSKEDKQGLVCSSEVP QNVGLQSSCPAKHGFQTPRVK KLYPQLPAEIAGEAPALVAVKP LLRSERLYPELPSQLELVPFTKE QLKILEPGSWLENVESYLEEFD SMAHQDRHEFYELLLNYSRCR KQLLLAEAELLTLTSDCQNAKS RLWQFKEEQMSVQVF
3685	34053	A	3725	182	771	QTALSCARHGRSAAFVWRPNR APVWRSGFRGVAAGSALVHST ALPSRRQPPERRSEHDCLRCRA LCGTKPQGLSY/TGP/WGLGKV PEAAAALDLGVH*PLFHLPLLD SESRKPGRGLAAPPPMPARWGL SCLEQVGHTRKEGGGQGCRPW PPCWSPVSGTRGGPITTRLRRGS AALHVRASYCLMENPPEPPSIV
3686	34054	C	3726	769	981	
3687	34055	C	3727	70	197	
3688	34056	A	3728	1	158	LGSVSSFASCTLGAPGYSPTAP VAL*SVGPWGRIVKVPGHPGS WEMHFIISM
3689	34057	A	3729	229	496	VTGLQNLVLSIVTESGKTHLLSF SSHGLEEIISQLPGCSGTLTVRP QGPT/GSQGNRGCDRVAQGSQ GAGGERGDRSQAPVPAPARDS
3690	34058	A	3730	167	769	FLTRETGDPTGRSSSHGKHPVA VFP**PTRPP*TIWEITHGCGRR AGRCPGTGPDGP\SGRGGPRCW PSGHLAATGGLGPSCGRLGAN RGEAGPAGFTVCSPLSGWRTPY THHFPASRMSWHLDYASPRTY RSQGNRGCERVAQGSQGAGGE RGAGSQVPVPAPARNKDPAKR QKPRPPLLSSPTARLIGLFPRAD SCRSC
3691	34059	A	3731	234	543	ALDQVASLPIMVPASKQNTATS CCRLGYNSFDLGPAAATIFFPSP AMVISQLPGCPGTLTMRPQGPT /GSQGNSGCERVAQGSQGAGD ESGDGSQVPVPAPARD

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3692	34060	A	3732	1	3695	MGKRSFERVLVDKCDSGRSCL RKQHENECAFIQILDTQSLMIPG QRGSFRLADSQHTDRVLCTLM AEKWDRKALSYTRNSFRAQIRL RKTRFQGKGCMICKKSRVLPY QAAYVSQHGSACQPSSHLPSVG SLSSTGDDEEEEEIVHMGNAIM SFYSALIDLLGRCAPEMHLIQTG KGEAIRIRSILRSLVPTEDLVGII SIPLKLPSLNKDGSVSEPDMAA NFCPDHKAPMVLFLDRVYGIK DQTFLLHLLEVGF
3693	34061	A	3733	1	2523	MKQFLLYLDESNALGKKFIIQDI DDTHVFVIAELVNVLQERCHTR LGYTEFLVAWRVTFGLCVEAV TLHLKYQILIRGLLEMMSFSDA DILKQLPVTVPGLFPASLSPSSL LGNSPPSWLRHNSESKVSAVSS PSATKTLSTGIGKLDPGHKEMA EESELLKNKMQAPPLSRCPESQ KCQHQLRLHHWKPSVRHQVKR RSPAVLRSAMPPADCPAVLEAT TATHPEKGTALSKHLPSSDSMS LKVDVEALENSPGATYIWKGG KVTRDSQPKEQGKGDLKKKKK GKLPKNYDPKLTPDPERWLPM QECSFYQGRKKGKKKDQMGK GTQGATAGASSELDARKTVSSP PTSPRPGSAATLSASTSNIIPPRH QRPAGAPATKKKQQQKKKKG GKGFPVLREITVVKVDTLVVFQ ILEERLSVFHIQYDTSYPFSTVDI EDHECAVWLLLRKSKSDDKTT RLEAVREMSETHHWHDAEKAF DKIQQPFMLKTLNKFGVDGTY LKIIRAIYDKPTANIILNGQKLE AFPLKTGTRQGCPLSPLLFNTV LEVLARAIRQEKEIKGIQLGKEE VKLSLFAGDIIVYIENSIVSAPKL LKLISNFSKVSEYKINVQKSQAF LYTNNRHTESQIMSKLPFTIATK RIKYLGIQLTRDVKDLFKENYK PLLNEIKEDTNEWKNIPCSWVG RINIMKMAILPKVIYRFNAISIKL

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3694	34062	A	3734	1	6208	MILDQAFKYITELKRQNDELLL NGGNNEQAEEIKKLRKQLEEIQ KENGRYIELLKANDICLYDDPTI HWKGNLKNSKVSVVIPSDQVQ KKIIVYSNGNQPGGNSQGTAVQ GITFNVSHNLQKQTANVVPVQ RTCNLVTPVSISGVYPSENKPW HQTTVPALATNQPVPLCLPAAI SAQSILELPTSESESNVLGATSG SLIAVSIESEPHQHHSLHTCLND QNSSENKNGQENPKVLKKMTP CVTNIPHSSSATA
3695	34063	A	3735	164	415	EYWGWLLRRINIILTGNCLRG/ WPSLLPQAEESLSPQTKVERLK AAWIEEGILPLLGMRKLFLLAR KVHQSLQAQCPQLHQGPPT
3696	34064	A	3736	1	886	MLDLPWFNVEEGIQRLREIGML EWLSHFRPTRLSREDPEDIPFTN TLPNKFVRGVPASLKSSFIGLLC MPDLTKTVGSWRMTVDYHKL NQTVTPIAAAVPDVVSLLEQIN TSPGTWYAAIDLANAIFSIPVHK VKDKLLHLAPPTTKKEAQCLV GLFGFWRQHFLHLGVSLWVIY RVTLKAASFEWGS\EQEKALQQ AG\QAAVQAALPLGP/HKDPAD PMVLEVSVADRDAVWSLWQA PIGESQQRPLGFWSKALPSYAD NYSPFERQFLAYYWALVETERL TMG/HQVTT*PELRIM
3697	34065	A	3737	1	1815	
3698	34066	A	3738	1	988	MPAEFFQRCSVIMVQLPWKEA HVERPHGERDYTPDLQPDMWE KFPGLRRALRPVVKTLLVQLEY RQAEKCEKRDWPSLPDYIFLLC WMLPALEYRTPSSSVLELRLAL RAPQPADSLLWDLVIVPITSLKS WQTPRGEVEGVTHEEICASLKS LAVALLSMSDLTVGTPVTQPQT LNTMGIIGSRGGRGQVAALNR QRQVPELIIGIDILSSWQNPHIGS LNGRGYINSLALCHNLIRRDLD RFLLPQDITLVHYIDHIMRLDSV KDKWLHLAPPTTKKEAQCLVG L/FGFWRQHISHLETAL/RPVTG LWWKLNI*LWAIKSPCNLNCLS
3699	34067	A	3739	26	318	RTAWMQYSPLHSAYGRVPTVT SSH*LLPLRSHPRDSRPAPCP/RA GPARNRQSSA/SRNRSPRRRNPE ASRGRPPGRGVASPAPSPPTPRE TRTAATRRP

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3700	34068	A	3740	425	588	IWSVPFAPWRRRGHAGSRCSRR SRSR/TPRRNELSTAALGAARG HARIWREAGNWP
3701	34069	B	3741	465	1623	
3702	34070	A	3742	667	960	
3703	34071	A	3743	1	2021	MTVLTQTSSQHSTGCHAKPAIT TPWLLAVFFQGPGVLQSVGGK ASQADIILGLSPVSAIFQLYDVS FPPGKQGRPGLGSAGRIEVARD CGMLWKQRGYLISSSQPIKNGQ QVSDLFEAIPEPKSLAIIKISGYS TLETPESKHNHFTNTLAAIDLV NAFFSIAVHKV\HQKQFAFIWQ GQQYTFTVLAQGYINS/PPALC HNLTQRDLDCFWLLQDNTLVH YIDDIMLIRSSEQEAANTLDLLV RHFCATGWEINPTKTQGPSTSV KFLGFQWCGACQDIPSKVKDK LLHLAPLASKKETQRLVGLFEF WRQHSPHLRMLLQLIYQVTRK AARFEWACTDGLMRSPYDQLT KEEKTRARFTDGSTQCEGTTQK WIAAALQPLSRTCLKDSVHQR VSSAEEDFNNQVDRMSRSVDII HPLSPATPVITQWVHEQSGHGG RDRGHAWAQQHGLPLTKADL AMFTAECPIFQQQRPTPSPQYG TIPQGDQPATWWQVDYIGPLPS WKRQRFVITGIDTYSRYRFAYP SFNASAKSTIHGLMECLIHSHGI PHSIAFNQGTHFMAKEVWQWS HAYGIHWSYHVPHYPEAAGLIE LWNGFLKSQLQYQLSDNTLQG WGKVLQKVVYALNQCSIYGTV SPIARIHGSRNQGVEVEVALLT VTPNDPL/GKY*LPVPVTLHSDR

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3704	34072	A	3744	3	1197	TLGPGTGPRAGTGSSSSPSSSPG TGSVPGAGPGANSVVHPGADS GVRAGAALAPGLC*VKLLGQM SPPGGALGPHNARQSAVAGGF GRARRPGRHE*LQGTWWSGPG QPLGAALQTATGPVVMNQFLR *TWHHEGHSRAPCPRFWGWF* TYSGEKPLPAAVQPSSSSVF*SL QQRCPFFLGVPCQACSSACPLL F*GL*W*PGVHEDQ*ASPAGSA LTWP*LHHDPPPSSGA*SDATG PG\GPGSALAGFQQLGSGGQVL QQGQLGSQTCRGGSPRGRRHC* ASSWG*G*AGRLLPWA**PPAR SAGSPHRLRGLS*ARPCGCAPR CRAAGGAGP*SSAPRT\GDGDV GQLGERE*EAHPARVGQWGW GSRCPQGQGVAFSGSESYMDW SSRNRRFRNT
3705	34073	A	3745	1	98	
3706	34074	C	3746	439	1053	
3707	34075	A	3747	48	751	EGDLVFPLGRGMLRLVSFSKMF KLLKRTMDYGSGSPSVSGHIPL PQACGPPQLVCSRRVRGQRPRP HSVPGSRAAPGLSGDTGRFLSG FGKFCFGSRKGALLTKGFSVSS GWPAAKFPPAQRVQTIVRSR\P RRPGKRVL*GEK/GEWAASLPT PLPLAGPSLPSVPGPVPVAPQTV RAVSPVTPQGPSSPPFLREHSTQ PRPGCREIYQHPRMGTGRMRTP WPWRLSARPAAAAA

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3708	34076	A	3748	1279	2791	QAAGGAAGAERDEGAGVA/GA HGPSRSTARRGGRGAGPRPPPP PRSLGTGSAGRGAAEGTGRAR RPAGAAAGRALRAGRAGRLGA CGGVAAVGARGLRAAAAGAR RRGAPATGAPPP/PSAAASPTAP\ PGPRHPGRVSGAAARAPPGTAP RIGERRPGGGAPATEPPDSRTPA AARASSA/PGAVSGPAAAPGPP GRRENAEGR*PQDAG*RGLWE GALPVPGSSPQTSSSSTGRTSGG SRAPSHMVPGTGSPPG\RGGEA GAR*AAAPAGVKPSSLWKK*L ALFRPCFQEPTPG/SVGCRGPLE CFTHSSPVGV/NGHRHCDNCCR/ PLKPPSPKAAWAVPRAAVPEA HA*K*RAEDQRGLRVLGPNVTL SNPPTRGFR*LGTGVPGFQDPC VDS/GL*VEEGLCPEASRGNGE RNKGTWGIPPQPPLRPSSRWLQ E*PTPLPGSP*DATSPPAGGGRH RSRLPKPALVGNAGTSSLPAPE PCFPHLYFTTFLLSLDSSLKFRD LAGILIPE
3709	34077	B	3749	71	285	
3710	34078	A	3750	417	1208	GPQRVPTLWWEDAEARSQRDG VGGRAEAPGARIPRDLGAAGG LRGHPRLVRGHCRRRLRCSMA RTLVLRVTPVPGGAPLALRQPP VPGGSRQEWPAFSRVGTGLPLT PTAGPSRARGARRPCPPALPGH CLLDRTYTGLQTLGAETLLAVV NSAAMNVGVQVVDVELHRHS LGEDCIYPQSSESDISDAPPSLPL TIPAPVKASSPIKQSHEPVPDTS VEKGS\PGSCPFHL*GPLSHLGS SPGFLLWRPPGLLSSVALVASC

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3711	34079	A	3751	10	932	LQLCSMWLLRSWVQAEGAVSI SDSPFSLHQCWAVLHKAWCVF LQLPGGFTFTLNPLSDNLLGKR VDSAPSWGPLGSAFRGVHMPC VGAAWEGKGPNLLRPSGKLGP SGSRPTPIGQQQLPEVPRAKGPL GPAAVICQ/HMPAPSTGGKRGS FSGRYLSASLELGGLPMAPTGP SALSAPPSVSRGAR*STREKPGV YASAT*AAEIREGQALGG\PRPS RNG/SGGPLGPDFGPNGPKLRRS KAGCPWWHLSSVDAGE*LWK QHSTAVFSMPGTQPPWRGLITM PISPRGTEPTAHPGPRSPGLAYS LTA
3712	34080	A	3752	3	650	GTVLDDPHLTGYCWHPPCPPNS VCNGSLSPVLREEAESSEAPVQ SPQRSWTPSAKSPPLPASPPCSQ LKAGGDQEGLQRGALPVGMD RGGPGGCGGHCQCSRPRILSPV VPVPQVCPSSEAPGPPRQVPHTP RPQEPSRTRGRLEA\SAPSWQ*P APPAGSLPAWP/PG/RPAPTGSR AR*AGLEASETTWSTNGPTTVH P*TL*AGSLGAPQTSAAASEHSP CPNLPLPL*KPWCATNLSCRI
3713	34081	B	3753	1	1812	
3714	34082	A	3754	1	209	MAQDYGAMGDLVLLGLGLGL ALAVIVLAVVLSRHQAP/C*PPA FAHAAVAADSKVCSDIGQRTC RDATPT
3715	34083	A	3755	2	462	PPLPGCLGDTGAPWPGPGCTGP PPRTRSPPRLPG*APASRLQNPH PRGRPWPAGHSRCH*SQPWLA GPTGS*HLPDASGFCPGALTGS CLPSLGGAGGGW\QSAPPDVGS KWNTPRRSGAPAPPGGRLLPGP ACRAPPRSDLPLS*AGRVGRPG
3716	34084	A	3756	129	616	NRIFLNCNMVHKCKCKTPMVV AGASLVETGQDESIKDE*LNGIP GPVATPSRLPPQRTWN\PGPHP MP*RRPQSLPQPSQAPPGPFLS* GSEGEGTQPKP/P/GLPGLGPPR QPGRCGFAVD/PPRCGVSPGPG VPGPAGPAAGAAPG*PKLRQRP GPSIGDCGDAP
3717	34085	A	3757	59	292	YCNVSFGPILSARKPASPRSS*T SATWLQNHPLMYLTPGTGTLW RFLTTRENVPYGPVP*WNRTIC GVANWPYWPSV

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3718	34086	A	3758	177	448	GTGGWVAMLQQYFA/TAWIPH NDGTNNFYTANLANGIAAIGY KSQPALWVTGGLLVIIITFIVRGI VYPLTKSQY\TSM\AKMLVL*P GAEGL
3719	34087	A	3759	1097	1206	
3720	34088	A	3760	2	505	QGSRAKLSTPLGLSCTRSTAGP SRFARCSLGGCSHPSRHSPHLPP PPPVQFRAGPRGRQGSPSRGSPS \GAFPAGPGGAAAAAVGDDQQ QQEQHGAHEGEENNEGNSVPC G/PGKTGGSSVSPGLPEPWPPAP LWTQPSWSAPCH\P*KPPIPPTR QVLGRTGCFLLPAP
3721	34089	A	3761	181	581	ADELNVPLT*APAIPLSKEMKL HVPTKPARKRLKWLHSQQPTC PSTGEPVSNCG\PPPVPQPTTQQ YQGLDAGATTRVPRSLLRSEGS QTQKSPSCGSHSQDNSGG/SQSS PVTPQHLLSPRAPQAAPSPDRA PV

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3722	34090	A	3762	18	2104	RWQGDKRDSA*RGNLRARKPS KRGK/DR*RRVSPTRSGKRRGA EEKNRQEKKKGREKERREKRS ERQRDRRRRKEQRKEEQRRRA RTNERKPRQTQANGATSS*KAS AQQAGMWGGSP*TDATAIRRG GAPCSSRRTCLNQGTIATPSGR\ RRHGDAG*PGLASEHDASGHG CLRTGAG*PSDSTESVCRRPLA MHVPTHESHGPVFTRLVSHTFH CG\SKLPAVGRPVACRPTYSPSL CHNPQRPAQLLAHSSALQCAPL SWDPQRCAPPSPRPHRRGPPSP HPHRRAPPSPHPHRRA/HTTART DPTTSAPPP/RQTQRRATREPAT KHTRNAHPRRSACNRGTHTHP RRRRTTERTTHHARPRNRGQAT PNTRQPTAGRHEETDGATRRR QHGQTRGEGG/RRRGRAAKTR QRERQEPPHDNTRRTRRRPKRR DRTGAPAGTRNRTSGHKKRQP GTRASTGTAPASQQQQTPTVLS RCISRFGVFYGPDFSGG\NSFCS LPLMSDSTLSTYGGQRRG/RSR ARKTQDTGVLSPLRRERSCPPA HGRFPGLFLSTHRQVGPAALRP PELSCE*LPQDGDFCVWLPSLR SRLRGTRVVAPASSP/CGDWQV TAVAP*PQTQSPSLSQSRDVEK RHRGQHPSVGSV*LMKAA*RG PSGAKRPKTAPRPQCRARVLPK RSGPTSPGRGSCGSQSRTRGF*D
3723	34091	A	3763	1	446	MWESLELPRDLLNGFDQNADN DMDNEIQAEVVSDGDEELVGN WSKGKQLKSSENLQLDDATEK KNLFSEEKFKLAEETYLSNEEP NINSQDNGKNVSKACQRTLEQ AFPS/SGS/GGLGGKNGFVG*AQ SPSAVCSLGTWYP\CPSCCSHG
3724	34092	A	3764	186	529	GTCWKLEQSTLPLLHWAGLAC PLAPGTCTSGPLL/TAPQR*MQL CGSPGWHWKRSVVVAPGRQLP GSGECMFQLPLPCRQPSLCAIPP ILQANLPLNGRQNCCAQISCKE DQSFH
3725	34093	B	3765	73	1374	
3726	34094	C	3766	1	873	

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3727	34095	A	3767	603	1208	FTTCSKHQTRPGHRPEQQHPAE KSVSGIFCYAEEMESSQLPDPGS GQPPRGG/ALGPPYEPLSNRIPD APG/EAGPASTPGH*SLDQGIPG *PGLAPRGHRLWKSPETPAPSP APRGVSGGLPGSRSAQVGSGDP SPHHL*QPAAAGRKDSSSF*AT WRPP/GPPGPAAAAGRKDSSSF* /GHMASPRPPGPAAAGRKDSSS FMVLP
3728	34096	A	3768	872	1015	VIRSRMLIPKTMGKVSPGHVRG LHSRPSQHRPRGLGGKNGFTAA PAMAEGSNI/GALAVASEGASP KPWQLPCGVEPS/IRRCMETPG* PGRSLLQEQVPHGEP/PARAAQ KGNVGLEPPSTVPTGVPPSGAV RRRPPSSRPQNGRSTDSLHHAP GKATS/SSMPAPESSYEGGGTL QSHRGRAAQDHGNPPLASA*P GDLVKLQLLTPQSDNSCTHIGD NGTYRSQLKAAFAEKLNMGKL TFFITGVNHKWGLPLSLTWLPA NSWESLLSFPPPSPPQQLNDKPG RRSNITHSSKEDKKTEESLELPR DLLNGFDQNADNDMDNEIQAE VVSDGDEELFGNWSKGDSCYV LAKRLVAFCPFPRDLWDFGLER DDLGYLVEEISKQQCIQEVTRV LLKAFSFIRETDHKSSENLQPDN AIENKIAFSKKKFKPVAEICISN KEPNVNPQDNGESVSRACQRSS QQALPAQAQRPRRKKWFHSCS
3729	34097	A	3769	234	636	GPVSGHHRVNCLPCTILPLRR*R AKGHLCRLLCPAGEATGARWR HSPQPLALLQRAPEPAHHHPAA PPGRLHHAGLRCSPVRPAEEGR GPRPQQRARTASLQLLRRR/SLL QPQPPD*\RDKMAEPQRRSRQP AHL
3730	34098	A	3770	1597	1878	DTPRFHSRSKRGITLQEYASSRN *RTSSAVPVF*RMSVRGMEVPC SNER*TQSISGDQVRPAEEGPGP RPQQRARTASLQLPRRRYFLQP QPPD
3731	34099	A	3771	97	471	GVEELRNVNVFFPHFKYSMDT YVFKDSSQKDLLNFTGTLPVM YQA*ICHCWSSSSSSPQVSRGTS HVFSI\TSDEARQVDLLAYIAK\T LKVFQIQIQRAGQIMRIKQSIKL LWLEVENSVLPAH
3732	34100	B	3772	1	1449	

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3733	34101	A	3773	1	927	MQRWFNICKSISVIHHINRVKT YMIISIDAEKAFDKIQHLFMIKT LSKIGIQGTYLHVIKVIYDKPTA NIILNGKKVE\AFPLRTGTRQGY PLSQLFFNIALEVLARAIRQ/EEI KGIQISKEKVKLSLFAGDMIFYL ENPKDSSKKLLELIKELSKVSRY KINVHKPVALLYTNSDLVENQI KNSTPFTVAAKIIKYLEIYLINY MKDLYKENYKTLLKKIIDNTN KWKHILCLWIGRINLV\KMTILQ KAINKLNTIPIKILP*FFTELEKPI LKCIQNEKRAHIAKARL/SQKN KSGGIRLPDFKLYYKP
3734	34102	A	3774	1	639	MGRNQSKKAENSKNQNAFSPP KENDSSTAREQNWMENEFDML TELDFRRSVITNFSKLKEHVLTH HKAAENLEKRLDKWLTRINSV EKTLNYLMELKTTLFMVDNG/C R*LENSHDL*AYFLHLLGNTGL *CCVRGQIGDGKEKREQRDSRS MG/EILRAQLEPFAFHQRSVQC GDIRDLWMGYFLLNLMKKLTF Q*FP*QDT*QLKELKKIAST
3735	34103	A	3775	3	1079	APGPRGAGAQKACGASAGGDP ECAAY*GGAQCECGPTVGPGE VPRAV*VWVHGGPWAGGYPV Q*CDAGGREGSFAGAAAAPGG AAGEPAGPCPGAAAAEPAGAG AQQPPAGREVCAGDSGPGAAP EAGGAGGGGAGGTAVPGGDPR AAAGPASGPQGPGTAAAAAGG RARGTAGAAPRPQGQHAGTGA GPPGAAGPARAAAGPAGQRGG TGGGPAGRA*TPDARWASAAG PGGGAAEASERARQGSDAAGR VVSGAG*AAG*TRGATGPAGA AGAGAGTAGDAEPAAARVQPA AGPERLPADHAV*AIDTAAKCP GRGEPAAAG*SSGPEPGEQGAP GAQPGESGPPAPRTAGVPGPA
3736	34104	B	3776	45	149	

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3737	34105	A	3777	3	442	EGKDERND\GKDEGKDEKKNE RNDGKDERNDEGKDEGKDERK DERNDEGKDEGNDEGKDD*KD EGKDEGKDEGKDDGKDERKDE GKDEGKDERKDEGKDEGNDEG KDERKDERKDEGKDEGKDEGK DERKDEGKDEGKDEGKD\EGK DEGKDEGKDEGKDERKDEGKD EGKDEGKDEGKDEGKDEGKDE RKDEGKDEGKDEGKDEGKDER KDEGKDEGNDEGKDERKDERK DEGKDEGKDEGKDERKDEGKD EGKDEGKDAGKG
3738	34106	A	3778	459	660	VRGHEWAQKKYHKFSLWSVD ST*N*QPSPHASGCHWLEEPAA FCHASPAASGIFAAAASDRPLLP SV
3739	34107	A	3779	2	440	RPLSLINIHANFLSKILANSIKQC LNRIIHHDGVRFIFEM*E*FNIHR SINVTYYINRMKNKNMII\DAEK AFDNIQHPFIIKILIKLGIEGT*LN TIKALLMAAAACL\NSCCKDAR SSRGGMAEGCRLSASSELWAP MSMGGGLR
3740	34108	A	3780	1	1145	RHPGWPTPAACPTTLRWLKAP VWTPGP/QKMEKEPAARGTPGT GKERLKAGASGFAGGMGPRSV PARKKAQTAPPLQPP/RAAPGPE RGAALGRPVAQQVPGARLAGG AAGLGFPAVPRVLPPFPCALSG DRSARERPPGALLRPLPC*GPPT \PVVGGKNDQLKERADSGPDPV AADAVPGEAALQARVP/GALGP AKLSPEGAIVAPA*VRGPGRLH QPGLRPGPRQRSDPRFPGSREPA /GERGRGARRGHRRGRPGGPCD PRRPGTQGEASERGEAAEGEAA EGGET*ER/GGRGKRRGHGPPG SPGKPYPSAGSHAKGATGRGH GTPGTPSPGRSRPGCPRGVPTRS SGLGVARSSAQARGGTEPAPRR SPGAPSGRPATLAK
3741	34109	A	3781	218	376	TRNKILYRQANAERFCHHQACP KG/RS*RKH*TWKGTTGTSHCK NMPNCKDHQG
3742	34110	A	3782	2	187	FTFWHDFAAAGTGCSFPCLVLP SWW*QNLSAFACL*RILFLLHL* SLVWLDMKCWVENSFL

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3743	34111	A	3783	1	220	IALMVSTIWHVFAVAGTGCFFP CLVLPSGALVRQA*W*QNLSAF ACL*RILFLLHL*SLVWLDMKF WVENSFL
3744	34112	A	3784	713	997	KFFSLRMLNIGPHSLL/CLQSFC Q\RSAVSLMGFPLW\EPDLSLW LPLTFFPSFQLW*I*QLGFL*LLF LRSIFVAFSVFPEFECWPALLD WGSSPG
3745	34113	B	3785	1	1698	
3746	34114	A	3786	948	1121	
3747	34115	A	3787	1211	2437	LTKRWPGTNTSPESG*SRRAAC AGL/LIPFTSRSSSPTWTRPLLS/ ACASSHDPGHHNSP*VLVPPDG GTQGFLVLHQADDLHRFLIKILI DIVRQRRENGVKILLGNRVMY HEHSPQVRGGQQLEQLPLITVH GGGLQLLHHVLSEGHSAVQNW GWTLPFIIAKLLMNLH
3748	34116	A	3788	1	1908	
3749	34117	A	3789	1	1788	MTGVSRGSGLPISMAENRRPLP VSAGSKPVIPILQSPLQILNTTH YFLKSLLTPTSSFAHVISSAEDL VQRRNVIGDVYSQGPASPFEIN NGLGSPLKYTAWRKQEMGPW QWLWQQDFHLFLGAPLQRYAE PLPVGTISPGWGSCVVDSSQES LPNDKHLRAAKEVPLQLQWQR SFQLPLGASPQRNTRILLTGMFS WVWLNIHPGTLLGEKLGSWGS KGRTTAGAIAERLLVSSESSIPG NPEQLPRNAELPLTEVFRCG*IFI QGPCLVKSWGPGAARAEPLQE P*RRGCWFLLRA/AIPGNPEQLP RNAELPLTEVFRCGQCSYAAGT PQKAPCPVRSSRARDPCRKPSD CLLGTDEQKDSSNLCRLKCPCL TALKRAVFLPARSWRSENGQT ASSSGSLSPEQPKWEAPPSRGRL TPHTAGSLRSQCDQREEWVSA MEDEMNEMKREGKFREKRIKR KEQTLQEIWDYVKRPNLCLIGV PESDGENGTKLENTLQDIIQENF PNLARQANIQIQEIQRTPQRYSS RRATPRHIIIRFTKVEMKEKML RAAREKGWVTHKGKHIRLTAD LSAETLQARREWGSIFNILKEK NFQPRISYPAKLSFISEGEIKYFT DKQMLRDFATTRPALKELLKE ALNMERNKRYQPLQKHAKM
3750	34118	B	3790	116	885	

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3751	34119	A	3791	593	883	
3752	34120	A	3792	47	716	EAPACL*KALSPLAPTTISSVDC GFRASTGITLLPRTGAAHGAAG *DRGGRAGVLTMTASRACCAG P*SS*RYLRQ*TPNSLEGPTGRS LRSRASPGF/TLRDPVTQPSSPV AAVS/ALGVEPGLAPAL*SQRV* ALPR*TRRKSKATAPTATKPNA GHNTTKKARPGQGPTPEIPALG SPREVDPEVAHPGAFLSQPERR RCVLGSSFPPGYQQRRVDPLPV
3753	34121	A	3793	2	829	GTRAGWRRRRSGRDGPEVTPQ PPGAARDGAG*TGPSPPRCAGP A/TAAKPSGHPPPGDFIALGSKG QANESKTASTLLTPAPSGLPSER KRDAAAALSSASALTGLTKRPI LSSTPPLSALGRLAEAAVAEKR AISPSIKEPSVVPIEVLPTVLLDEI EAA\SWRATMTGSRACCAGP*S S*RSPAPSLTAPST*ASCTWPRS SPTSSPLRASLRLCVASCGGTPP STSRPRGTAWCLCWPVTSSWPP TRRTRTGPRSLSRCTSRTPWGS GSGWTALT
3754	34122	A	3794	114	254	
3755	34123	B	3795	1	2052	
3756	34124	A	3796	860	1090	
3757	34125	A	3797	2252	2557	LNPLSMGRRWPGEETVTDPGW KRLCHPLHWVAETVPVQAVGA PWSLQMGGWNWGGRCPQHLA PSKGVM*RLPGQFGRTPSWKE VPEVWGMFRRPACGPRLS
3758	34126	A	3798	444	854	VSHLEAQK*PSWTC*HQCQWA LPMFPHHSEADGLIE*WNGLLK SQLQCPPGGNIL*G*GKVLQES VYAQNRHLIYGTVSPISRTHRPL CSQSTQDSCLLVANPSQICLVHI PFP*VQHSLGL*ISWDWTGEVG PFL
3759	34127	A	3799	1169	1881	LEHPATVIFCFSWETFDPQGFCF SLPKVSGTCLISLLLHAFPFVVT SAPCPQEFPHSPHLCFHVP\HHS EADGLIE*WNGLLKSQLQCPPG GNIL*G*GKVLQESVYAQNRHL IYGTVSPISRTH\GHQVTHGQPV KTT/LL*SPSMGSWGIALVLPPL\ DLLLSG*SLTLPLAFLLRTHPLL TTVQRRAELPFTSWICFLSLFER GKGPGQPLVTWTECQALTLLPS PGSHTQGTWRIPH
3760	34128	B	3800	65	1324	

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3761	34129	C	3801	1	1263	
3762	34130	A	3802	1	2845	MAPRSLRMEDAIESLAVVSSEY VGAGVNWMFLPPSSKSTCKILT PHVMVLGEQGLAPPTVFLKALP IPLYHTVPPGGLQPRAPLVTGSL DGGNVPFILSPVLQPEGPGPTQ VGKPAAPTLTVNIVGTLPVLSP GLGPTLGSPGKVRNAGKYLCP HCGRDCLKPSVLEKHIRSHTGE RPFPCATCGIAFKTQSNLYKHR RTQTHLNNSRLSSESEGAGGGL LEEGDKAGEPPRPEGRGESRCQ GMHEGASERPLSP
3763	34131	A	3803	1	279	
3764	34132	A	3804	2	517	KGLAFEVSLADLQNDEVAFRK FKLITEDVQGKNCLTNFYGMG LTCDKICSMVEKWSTMTEAHV DVKTTDGYFFHLFCVGFTKKH NNQILKTSYAQHQQS/RQIQKK MMEIMT*EVQTNDLKEVVNKL IPDNIGKDTEKV/CPIYPLHDVFI RKVKMLENPGFER\MELRGGGS
3765	34133	A	3805	18	602	PAPWRLACNKRLTKGGKKGAK KKG\VNPFSKKEWY\D\VKAPA MFNIRNIGKTLVTRTQGTKIAS DGLKGRVFEVSLADLQNDEVA FRK\FKLIT\EDVQGKNCLTNFH GMDLTR\DKMCSMVKK\WQTM IEAHVDVKTT\DGYLLRLFCVG FTKKRNNQIRKTSYAQHQQ\VR QIRKKMMEIM\TREV\QTNDLK EVVNKL
3766	34134	A	3806	525	1173	GEPHSQATSGHFASSAGDTQAN RVWSGPPANTNRPAAEGHDC* KEN*ETERTSTPKPHLYVTIIKD QRKGISD*RSNE*NEARREV*R KKSKKK*TKPPRNMGLCEKTK STSDWCT*K*RGEWNQVGKHS SGYYPGERPQPRKAGQHSNSG NTENATKILLKKTNSKTHNCQI HQS*NEGKNVKGSQRERSGYP QREAHQTNR*SLGRNSTSQKRV

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3767	34135	A	3807	111	1329	RNRRRERHKEREGGGTGGTDW *RRGNRRKRTQRGRDDERRGR DDDQNHTTNTRRETTKTKRTT NRTQQKREQKRNETSKRNETK RATEQNRRERTGTRSGRSAKRQ RTEPERERAARRARAKRTASAA RDRGLSSTFQLPTRSGNSVHTS KKPLSRKYEQDPWADS/GSEGV WKPVPRRLEAKVMRESQGSSR SCCNSRTSARLITRTMR*ATLSS NKWSFCMPAGRCLTVTSPCCTP CALVTRKMLVTLGL*SRSRELT T*GTFVRGKQK\SVFSAAWGPG HQAQCSEQPSRGRFHRAQPMA *EPCCKSRHPRATPLHPRPSRPK SPTTPPPTRQNANNKGHNTTHT KPRAPPEPQTTQHEHTPQPPPDS HAQDNNNKNTPQQPPTKNAER PPRPTAHPPPAHKPLL
3768	34136	A	3808	2	517	
3769	34137	B	3809	1	1008	
3770	34138	A	3810	139	1407	WRGGLDSALRAAVTLQGCAGC DRPGSA*SNNYSI*I*R*RW*SN YSEK**GNEGNAVILLFHSNGT ASKWTVNRASADISKSLQASW GTEHTWPEGEYS\AGPSQHSSP AVSDSLPSNSLKKSSAELKKILA NGQMNEQDIRYRDTLGHGNGG TVYKAYHVPSGKILAVKVILLD ITLELQKQIMSELEILYKCDSSYI IGFYGAFFVENRISICTEFMDGG SLDVYRKMPEHVLGRIAVAVV KGLTYLWSLKILHRDVKPSNM LVNTRGQVKLCDFGVSTQLVN SIAKTYVGTNAYMAPERISGEQ YGIHSDVWSLGISFMELALGRF PYPQIQKNQGSLMPLQLLQCIV DEDSPVLPVGEFSEPFVHFITQC MRKQPKERPAPEELMGHPFIVQ FNDGNAAVVSMWVCRALEER
3771	34139	B	3811	1	1134	
3772	34140	A	3812	374	931	WRGGLDSALRAAVTLQGCAGC DRPGSA*SNNYSI*I*R*RW*SN YSEK**GNEGNAVILLFHSNGT ASKWTVNRASADISKSLQASW GTEHTWPEGEYS\AGPSQHSSP AVSDSLPSNSLKKSSAELKKILA NGQMNEQDIRYRDTLGHGNGG TVYKAYLCPEWENIICKGHTTR YYTGTSEANYV
3773	34141	A	3813	3	444	

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3774	34142	A	3814	75	807	GIAGFVNIHLDSLSFLTGVPGVK AERF\E*RMTAKHCALSLVGEPI MYPEINRFLKLLHQCKISSFLVT NAQFPAEIRNLEPVTQLYVRVD ASTKDSLKKIDRPLFKDFWQRF LDSVKALAVKYLQRIGSRTPM DTKIYSYCPAVHPAEPTDMKS WPSLFEVPTSLEYCPFYLQLVES ADAEGTQKYRRLTAYYIPVYTE PPLITKEPSCLWKQAEFGDLGK HVWLVEQFSSTRVQEHGVGW
3775	34143	A	3815	35	2088	KVMNKRSQTQNGTRYMTPPPR SSHTKQHLL\PTPPPRSSHTKQH PLHDPITTKLTHRT/CTRYTTPSP RSSDTEQHPL\PAPSPRSSDTEQ HPL\PAPSSRSSDTEQHPLHDPT TTKLTYRTAPATRPHHHEAHTQ NSTRYTTPSPRSSDTEQHPLHGP ITTKLTHRTAPATRPHHHEAHT QNSTRYTAPPPRSSDTEQHPLH GPTTTKLRHTTAPATRPHHHEA HTQNSTRYTAPSPRSSDTEQHP LHGPITTKLTHRTAPAT/PAPSP RSSHTEQHPL\PAPPPRSSDTEQ HPLHGPTTTKLTHRTAPATRPH HHEAHTQNSTRYTAPPPRSSDT EQHPL\PAPPPRSSHTEQHPL\PA PSPRSSHTEQHPL\PAPSPRSSHT EQHPLHGPITTKL/STQNSTRYT APSPRSSDTEQHPL\PTPSPRSSH TEQHPL\PTPSPRSSHTEQHPLH GPITMKLTHRTAPATRPHHHEA HTQNSTRYTAPSPRSSHTEQHP L\PAPSPRSSHTEQHPL\PAPSPRS SHTEQHPLHGPITTKLTHRTAP AP/PTPSPRSSDTEQHPLHGPITT KLRHRTAPATRPHHHEVQEQA KPIK*PPRPSPETTRAQPREPAV TLLPSGALGQACPCDATAGPHG TTLWPAVPPRWQQHLTRELLH PVPRACP*QGQGQPFTAGPGRG SHPYDPTGASPKGQSSIL
3776	34144	A	3816	83	184	RLTLPDRLGSPPDTH*AQHITRA VLPQGFTDSPH

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3777	34145	A	3817	1	811	MAEEDSGNLQPEGEGEAGTSS HGGAGERVKGKVLQTFKQPDL TKQTRFIRGPKTPAPVTDWEGS LPLVFNHCRDASLIIHPHFKGVR PRRDACLGPSPLAASPAFLGKG QHALKRLKPIITRLLQHGLLKPI NSPYNSPILPVLKPDKPYKLVQ DLCLINHIVLLPIHPMVPNPYTL LSSIPASTTHYSVLDLKHAFFTIP LHPSSQPLFAFTWTDPDTHQAQ QIT*AVQPQSFTDSPHYLNQAQI SSSSVTYLGIILHENTRALPADH
3778	34146	A	3818	2	324	HFEARRQAGPPKPSPQPPFR*LP TAGT/RGGGGEKAAGGFRWGR FAG/MGQGPDPPGAHGQNPASP SLDFPWGPICASQGVTDQSPSTF QGPLGEA*KPTAGAKPGAGAG
3779	34147	B	3819	206	1391	
3780	34148	A	3820	229	792	LGSSAGNSAPDPWRPTSSGVFS FHNTSHSHWILRLRTQERFSEV CVQGTWPTRPLWALPPP*FPFPS PAPAAFASCQSLPPHSPQSPRPG AGIS/RPRSQEAPDSSQ/PAPTRP SVPSPMANQGSGDDRQPPPPQD TPPRPNAASQSAGHNYASLPAP RGRVGVGIGFPGSPACAGGGIW HFHTLSFPAF

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3781	34149	A	3821	3	1676	KDNERRLNTCRSTRSHKRAHTR RSIRAHRGSAAAPPAAQAPGW RWASSCPRVQSAAGRGGRSGA ASGR*APRWGCPP*CGSRPGKC SPSPAPLASTFPRPGTEPPCRL*R GTCLGSACSGGSGRG*RR*GTG TQRRCPLPSARPRTRRRQISCQG KFS*CPSASSTNVCSPTGRGL*K PVPWAPGGRRRRPS*GRSSGDL SSGTWWP*S**ELGIPEYSHST/Q G/LVGVAMPPHRRAVTGNVHIA GQARKKDSP/GGRSPAWL*SPL FCAPGGRGASHLLLSFP*ESPAP *TARP/PLPARKLTVPVVLLRDG LGRGGLGRR*PCSAEKS\GRGRS GWRRARRPPSEAGTRGNRTSSS WRAPWRPGLGTGEPPGAPPGF APSSSPRRTPISPLSPASGSGGSG LGRRQRAADRARTKPGGD*VG SWAGRRPPGGAEGP*GQRRPRP YAVLLLSGWP\GGEGGGSLQPS VQLLVQGGPVGLTG*VSPRLLT REALKQNGATEAGGEHWPSCP PSH*/PGAGEHPGAADTLQVAS PA*GHGTAGRQGRAPAAHPAH RGQRAHSTRQ
3782	34150	C	3822	78	371	
3783	34151	C	3823	349	591	
3784	34152	A	3824	822	2114	AGRSVRIQAMTCLHPAHLGYP GSFQAPESSCPGQ*GRMHSQPT P/AGRRDMQDEPSFSNNIGVAG PGAMSRYTCPGCKNSNQRTEEP KKMR*TF*SLSSFPWGSGSPHP VPSFLWVPPSQLPNT*KLRAGL GTSGLAPGGTQKLRFMRASLW QSKKSRLCPRWGPSGPVGSV*G VEGVAE*RQGLGT\AGSGHQPE RTGHRLWPAASG*SLACSAPSR KGSCFSRPSLRSTETSLPAPGSL SAVGH*GVESAWPAAGRAGNH FGPEVADNLYEMKPPEPQVKP GLGRRQRAADRARTKPGGD*V GSWAGRRPPGGAEGP*GQ\GGP GLTLSFFFQGGQSGEGGGS/PAA ECISGGDSDVALQGSHCVHSEQ GCLAELEDPG*EPGVAVPGWG SQERNVAGTGGVSAHGDTACR PAPPGHW*PTGRGDEIVEAKTK

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3785	34153	A	3825	3	452	PRHSPGCRCPVAEGQSSGRALP PRLILLAVLLLLLCGVT/CWLCP VLLPPEAGTGPATSATSTAALR CGSHPYGQ*QPCTQ\P\GPPTAP CSTHWACGCPAFGSWNWTPW/ PPPAYSLYTPEPPTSYDEAVKM AKPREEGPALSQKPSPLLGAS
3786	34154	A	3826	16	118	
3787	34155	A	3827	292	1047	SWQELESRAQAPNVGQRDGPR RGLSYHVAAEVNELLVEGQHR LEGDKHFTGHSG*QGARGVKA AGRDP*\PRGLVKAVGRGAMES RSSSPKGRGNRMPSGYCTEL*A AGNQSGFVEAGLAFTPAIST\PT GGPLGTHRSQCCVQGCHCP*G* LPRRRAAVLVADVAGPVPASG GSRTG/AQPAVTP\QAEAGGPPA G*APLATGCSSGPRAGTGPRGR SCRPRSPAPPAAAAGAAGAAG AAAAAAVRGRSAAPGP
3788	34156	A	3828	2	462	GPVSIGEPEIGPPGPVSIGEPE*G PPGPVSIGEPEEGPPGPVGIGEPE EGPPGPVSIGEP*EGPP\GPVSITE PE*GPPGPVSIGEPEEGPPGPVGI GEPEEGPPGPVGIGEPEEGPPGP VSIGEPEEGPTGPVSITEPEEGPP GPVGNEMSSR
3789	34157	A	3829	3	374	YRALVFSSSTQ*VSKNFLYSGSS SMLPVLASFFLSFFLAIFWNGA NSATAGYSRPQVGGEELEVVV CWQRAQLLLQLLLGEARRQAA DDHLRGARGRSHRGGAWTRSS KGTAYRAGRPGPRPTK
3790	34158	A	3830	66	619	VRSLFSEMNVVEFQNGFWNMF PVKRPKISCSGRVCSIPEDSQKE AEKKRCQDWKHRR*SRI*EVFR NL\RVEEEKTSANPETLLGEME AKTRELIARRTTPLLEYIKNRKL EKQRIREEKREERRRRELEKKR LREEEKRRISVEDRWLYTIRINR RKSQRKK*GLRSHSGSDKEHRD VERSQEQ
3791	34159	A	3831	253	482	QVSTCYHSQEKEKKRISSTSKSL NKEKRRNEQ\KDQ*ALLSSPPSP PAESQGWHWSSLPPHSRFLKTS YILDLDIKK
3792	34160	A	3832	156	443	
3793	34161	B	3833	426	513	
3794	34162	B	3834	47	1311	

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3795	34163	A	3835	1503	1652	NCGNNQ*LTNQKKSRSRWIHS QILPDVQGGAGTIPSETIPINRKR GNPP
3796	34164	A	3836	1	1986	
3797	34165	A	3837	1	1116	
3798	34166	A	3838	1	546	ERSSSPAAEQSWMENDFDELRE EGFRRSNFSELKEEVRTHGKEV KNLEKRLDKWLTRITNTQKSLK DLMELKTTARELHDECTSLTNQ FDQLEERLISNFSKVSGYKIN\G KNHKHSYTPITDKQRAKS*VNS HSQLLQRE/YKYLGIQ/AYNGCE GPLQGKLQTTAQGNKRIQTNG RTFHAHG
3799	34167	A	3839	1	987	
3800	34168	B	3840	1	1593	
3801	34169	C	3841	1	1479	
3802	34170	A	3842	129	368	
3803	34171	B	3843	1	1884	
3804	34172	B	3844	1	471	
3805	34173	B	3845	1	675	
3806	34174	A	3846	1	410	
3807	34175	A	3847	250	880	GEVTKPQFAQFFHGSLASLTIRP GKMESQKVISCLQACKEGLDIN SLESLGQGIKYHFNPSQSILVME GDDIGNINRALQKVFYINSRQFP TAGVRRLKVSSKVQCFGEDVCI SIPEVDAYVMVLQAIEPRITLRG TDHFWRPAAQFESARGVTLFPD IKIVSTFAKTEAPG\A*KPQVQN SEFSL*AFENPVSCQISNSGHVP NFQFRV
3808	34176	A	3848	890	4889	
3809	34177	A	3849	1	799	MYAQPPNCKREKASGDVSLYW WKLAKGCLQMEVSEGAPNSAS TPTGNTVSQELNRPLP\QPPYPR RFSWVCRSSLQA*VAESATKTS AFRAPNSFCRLQPRPCCRASPAS PATSCTCPGSLAWARPAPASH WARPHRPPPCPTSPRP\PRGRDA PER*AHGPPVPDAR*GALAPQA TGGGQPPGAQPHHARAGPGQP RTPL/Q*GLCARPGEPQLRVTPH GPQAGG/HTQRLPPMGKPGVSG GVCPHSDFPQPMPTVEMTGPRS GVQRPT*DGTGWLAPDAESLV SFEFSSPT*VL*QQWK*RSGVQR PT
3810	34178	A	3850	212	361	

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3811	34179	A	3851	3	909	GGRQRGKDTGHMAKQEQERE VGGATHL*TTRFRSCSK\SALIP VIPITKSTGSRFRNSVEGLNQEIE IIIKETGEKEEQLIPQDIPDGHRA PPPLVQRSSSTRSIDTQTPGGAD RGSNNSSRSQSVSPTSFLTISNE GSEESPCSADDLLVDPRDKENG NNSPLPKYATSPKPNNSYMFKR EPPEGCERVKVFEECSPKQLHEI PAFYCPDKNKVNFIPKSGSAFC LVSILKPLLPTPDLTLKGSGHSL TVTTGMTTTLLQPIAVASLSTN T\SKTESLEEQVQSCHQLLYSHH QNQLRKLKD
3812	34180	A	3852	189	454	LWKRFNSWTSLRHPYQPYQAE QIAPQTCGSQSDGGLPSSSGPAP LHHAGLGYGTEGSPGARRRVE GQDP*VLEQAAGPTPPRYLVRP
3813	34181	A	3853	17	561	IPGSWRQKMPVPPAA\PAHAQG RPGALQSPGSSTPAQPGSRWEV GGPAAPWGSLRHP*QPYQAEQI APQTCGLQSDGGLPSSSGPAPL HHGGLGYGTGGSPGA/LEEGGR PRSLGPGAGSRAHAAEVSFPSG PPSRGLTGSGFCACSEERAGFPR ELMVIKNTVTPTREATTLILTKA PAILP
3814	34182	A	3854	1	540	FFQPIFWGKDPQSGTPPHP/RPG PAPSGPEPSISMVTRRWLRAPN CSDRRGEGPRTEADRHGSCCRF RSRAGTAVHSCRRRHPRAAGLP SSLCAEAGPRET**LEGGCREG AEPRP*RPGSGAHAHTDPERAH RSGARTQ/HPERAHRSGARTQIR SAHTDPERAHRSGAR\HRSGAR RTLPL

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3815	34183	A	3855	1326	2409	GRPPGVPPATAPRAAPGAGDGE AGTPAPGDHPEPVCRIQPG*WG T*GWGASQHWGGH\PALALAG RRPSRGLAGASGRSSEEPGVAT QRLWESMERSDEENLKEECSST ESTQQEVLALEEERAQVLGHVE QLKVRVKELEQQLQESAREAE MERALLQGEREAERALLQKEQ KAVDQLQEKLVALETGIQKER DKDLQRQCCGMMGDRAKASP SWTSTVILKFPLIKNCLNPKDIS LMAKELWSLRTMDALNRNQIG PGCQTQTMVQKGPLDLIETGK GLKVQTDKPHLVSLGSGRLSTA ITLLPLEEDCLPSLVDDLVPRLG LKISLETRRRGQLMLCTPKFEN QWPTTDKMPETSTGSH
3816	34184	A	3856	240	639	DHGRSQ*EPNRPWMPDPDHGA ERTLGPDRDRQRAE\MQTDKPH LVSLGSGRLSTAITLLPLEEGRT VIGSAARDISLQGPGLAPEHCYI ENLRGTLTLYPCGNACTIDGLP VRQPTRLTQGLSMSLPSQLIQET
3817	34185	A	3857	1	1758	MALLPTVLCLWAQAQVGVQR HNHIFWNEKEHGHGKSGSCHN GASCSAEDGACHCTPGWTGLF CTQRKPHLLASQPLRIPCCGLL ATVGIVQTSREGGMQAAPGLV VPDSCPTRTEELCRGSSRPDWIQ GIDKPKVLQGCPAAFFGKDCGR VCQCQNGASCDHISGKCTCRTG FTGQHCEQRCAPGTFGYGCQQ LCECMNNSTCDHVTGTCYCSP GFKGIRCDQGIMLLLFLIV/CAA GPICLASAAAEREGPRPGSPCLL HTCHE/R*PAPTTPSQDLTDHYL RFSMPIMVLT/CLQGAFPGSPGR \PG*TWAPLCGMNVNRPGT/HE LGCDSDHWGPHCSNRCQCQNG ALCNPITGACVCAAGFRGWRC EELCAPGTHGKGCQLPCQCRH GASCDPRAGECLCAPGYTGVY CHPVTGACTCQPGWSGHHCNE SCPVGYYGDGCQLPCTCQNGA DCHSITGGCTCAPGFMGEVCA VSCAAGTYGPNCSSICSCNNGG TCSPIDGSCTCKEGNVPSLPSPS LTYEHIPQVVLPAEGSQDGTFG LNCSEHCDCSHADGCDPVTGH CCCLAGWTDIQEGFLEKEGPKR
3818	34186	A	3858	2	2414	

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3819	34187	A	3859	1	852	DEEEVVAREEEEEEEEEEMVPE ESMASAGPEDFEQDGEEAALA RGAPAVDSLGMEEEVDIETEPV AHEKRPSMLDEPPLPVGVEEPA DSREPPEEPGLSQEGAMLLSPEP PAKGLAHPNGSQKVIFRVPLRV IHGPKAVELQVFPGLHKQPTNQ PK/TEPCDPHSWFKSCYHLLFIP VGISRPP/HNPTITATIFASTASV LW/PVLDTCMSSNSGYFKAVLE SYSSKVLSVTQYGNPRATGSAG LRGRPGS\PGSSGSRGPAWP*PQ AAPRCPPSSGRPGPTSQSPS
3820	34188	A	3860	3	1997	AQGSVVPGLFWAFLQLEVNCL LESPIIQGKFHFRLERISVVEPQE RKRLSFRKSEI*P*K*SLVKKL*E RLKTRKQMQLANRLRRYGYSV VES*FPNLKVSSSVSTTPTTTYIP MTHKAIFSSYFLWDGRSAFLTI YKMMSSHPQEEEEEEEEEGGE GEERKRRKKEEERGKRRKRRR RMK*RRRRTRKRRKRRKMK*R RRRRRRNMRKKRKEGKNMKK KM/REEIKRQNALYEIEMRKKL EKKREEMHESRRRFLAPLFSSP TANCSTSLVPRLRLASLPAALPS NRVVRVTTPPAGVRGAWRHSH FSRSRSIMDTSSEMLVRFGRRC GRAKESTGRDWNSLKSSEEDR KMWESLELPRDLLNAFDQNAD SDMDNKMQAEMVSDGDEELS GNWSKGDSCYVLAKRLASFYL CPRDLWNFEKDDLGYLAEEISK QQSIQEAQRSRRKKWFYGPGPG SLCCVQPIDLVPCVPAAPAMAE RGQCRAHAVASEGGSPKPWQL PHGVEPVGAQKSRIEVWEPPPR FQKMYGNAWMSRQKFAAEAG PHGEPLLGQCRRELWGRSSHVE SLMGHYLVELLSIGAMGIKVQR PRCFFDIAINNQPGEKGTGKSTQ KPLHYKSCLFHRVVKDFMVQG GDFSEGNGRGGESIYGGFFEGP AMGPNATNNFTKLAG

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3821	34189	A	3861	86	1120	LVLSKGKEHLLGIKEHEEEEER RKKYE*KDAEEIKRQNALYEIE MRIKLEKKREEMHESRRRFLEH MQDKHIIKAVEQQQ\RQRKKM KR*ENSSKQKKRLIQMGKEKEA ETHRLMEKRRERIHNFLSELLK EKLDNEDMIIARDIAEAEAEWE KREREKDEKNQAELKTIAEYRA IVMKNKEEEERQRKIEAKEQLL AVMKADQIFWEHEKEKKCKA DKEHQEVQDAHIQQMAKNKFN AKQAKQAELDYCRLTEALVAE KEKEFQDYAREVIELESETPNK YIYPLVKAVQEGPGGGRGPVFV DRGGLRPSYQANDVTGVQLPF YNSQGPKYNFQKSKRRLGFTW
3822	34190	A	3862	591	2805	WVHQPAGS*GEKPT*ISAPPWP EAPTSELWVLTPPEAVQEAAAR VGQEVPAAP/RGPLPSSATGAK SLGQGSPTPSTRSMSLQSCAGP QHP*TLRRGPLWGTSRWKMVL T*ASRTSSTPGLT/QGPRVTVLL GKAGMGKTTLAHRLCQKWAE GHLNCFQALFLFEFRQLNLITRF LTPSELLFDLYLSPESDHDTVFQ YLEKNADQVLLIFDGLDEALQP MGPDGPGPVLTLFSHLCNGTLL PGCRVMATSRPGKLPACLPAEA AMVHMLGFDGPRVEEYVNHFF SAQPSREGALVELQTNGRLRSL CAVPALCQVACLCLHHLLPDH APGQSVALLPNM/YSALYADG ARPQPPWALAHLV/LYWTWGR WP*GAWRQGRLSSMQKILLHP* *LLGPLTAC*LPSASAQALGTS/ ETGYAFTHLSLQEFLAALHLMA SPKVNKDTLTQYVTLHSRWVQ RTKARLGLSDHLPTFLAGLASC TCRPFLSHLAQGNEDCVGAKQ AAVVQVLKKLATRKLTGPKVV ELCHCVDETQEPELASLTAQSL PYQLPFHNFPLTCTDLATLTNIL EHREAPIHLDFDGCPLEPHCPEA LVGCGQIENLSFKSRKCGDAFA EALSRSLPTMGRLQMLGLAGS KITARGISHLVKALPLCPQLKEV SFRDNQLSDQVVLNIVEVLPHL PRLRKLEQGRSGAPGVGDSTPD
3823	34191	A	3863	1	2784	

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3824	34192	A	3864	727	1715	YLSKGLKEVREGSLQIPGEIIPG RKKLMQMLSEKTL*SQHHY*K GFLQRQIHQKMIAHLVEQRNK DCMFLQIMPAATS*/TEIQATIR DYYKHLYANELENPEEMDKFL DTYTLQRLNQEEVESLNRPITG SEVEAIINSLPTKKSPGPDGLTA EFYQRYKEEL/PKPCRDTTKK\E NFRPISLMNIDAKILNKILANRI QQHIKKLIHHDQVGFIPGMQG WFNICKSINVIQHINRTKDKNH VIFSIDAEKAFDKIQQPFMLKTL NKL\GIKYPGIQLTRDVKDLFKE NYKPLLSKIKEDTKKWKTILCS WVGRINIVKMAILPKAPLPLPP
3825	34193	B	3865	1	1908	
3826	34194	B	3866	609	1658	
3827	34195	B	3867	61	234	
3828	34196	A	3868	1	978	LFTDDLCQPVEATSGQAMVQS RGATTHGGGRGGSCKLLGDRG QGSTSQVGRWGSSCHPPTGG\P ARSPCWPTARKPLRGVLQGASL GSTASMLGAASGTPRPPPSWLV SVPSPRAPCWGVPGAG\EQGGP ETQPPGAREYPQPAGREGRPQI LRFPKSSSSQCLVEFCSLASSCF ALEAMKTRRSPSS/SGSSGSDG/ SQRTTRSGPAQRPRVSGSSEQG\ DGMRGGSSGGMKGRRVPKREP RTEAASSSTA*RQPPPPPSPLPH ARRHFRFRPCCGPARDAAPSRA QTEAPPPLRTQSALSWPLCSRT DGKLSRGQSRDGSRAPTPGVL

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3829	34197	A	3869	1	1919	TPVSDEEEGSLHHTTWRNLRIG VRIACPAGENAQSSESPVRACQ PGTKTQYGLNQAWSPGVRRDL IQGSAERPARYPAPGEMGVGAF IPLGHDKRRAASQHLHVSGREG PEALGSRGSALRKQVPAWLPHS LRTCPVDRNPQAPCARTGLMV ETPHHEQWVRGEHYRYKFSRP GGRHAAEGKWWVRKRIGAYFP PLSLEELRPYFRDPHTLMLGQR VTERELDGEPRGPVTVEGRSAT TSGYPTKVTKIGGPLDPAGGLE GPLHGALGSDPLEVSDCPGPHL SRKVWENGSFGASDQQHTR/YT TDGSSWPTVAEKKAPSSKQYH SSMET*R*TGHSNHPRNRPTCG QVPPNENNTRNRPTHTARYLPT /ENNPRNHSTHATRYLLTTTTTE IIPHAARYRPTRTTRYLPTRTTR YLPTKMTREIVPHAATYLPMRT TREIIPHTATY/ASNENNQYLPM RTTSQVPSNEDNPGCLPTRTTR HLPTRTTRYLPTRMTQEIVPHV AWYLPTKALRPFNGKRTAFSA NAAKRSEAPTLR*ALRT*CPVN PPDTEGTGPAMPSLECPEQGNP QRRWAGRRRSSGAQDAGQGTR FTPSLWRAWGWSRLRPRLSAP GCWLTRKCRTEPPVVPQALMM AAVTDMQTLIH
3830	34198	A	3870	295	457	
3831	34199	A	3871	296	1057	GNEVKMPARETTPHRVPTGAQ PSEAGEKGHHPPDRRMVDPLTL ALCTWKSCRHSMPDCKAAGRE AVPCKVTGAERPRPRAPTSA*P SGKLEGLSLWCTQSCSCMLHR AGVISVFFTMEDVAPTRGLLH* RAAIGIISPITISVTKTSNNCRWC RVGGCAN*LRGALEAGG/WLQ NQKGRDAFNKRLRGGMDKPG AGGTCGSGRRNRPLRDRS/VPE VKGGTGTG*KTGSGGLKRKYV GDGTTASFESLRVLIKWPL

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3832	34200	A	3872	3	913	GGADSGERLGPHALGLGAGSG GGRGRYGPSRSRPSGRAADPGG VRPFPVAPRGARARRGGRVVP AF*RPAGAA*AAQHHVVVSEP AAAARGGGGPGGQGSRAWRG VRRLPGGAGGLAGPPGRVPVL GPPGSGPAAQRPPGRGQGAGQ EPPPAGDAAAA/PSSGSASCR/G PGAA/GPRALCPGPAPPARRGPR AGLGRPAADRGAPAAAPVRAE PHGLGGAAGARPPHRLRGGAG H/SGALVVLLTLWITGGGGDGD RASPGSPGPLAT/GAGLVGNKA APS*RAARAPGGLGCRWARFSL TSQCPCPQL
3833	34201	A	3873	2	484	TPWRRKSTE*PTLGVRRPVPRN AMPHHCSFFTGRTVPSMATPG YNEGWDKFRMKCHLCVNYIE MQTDPANCDYVIVSGAQRKEE RWDMADNEQVLTTEHEKKQK LETDAMFRLEHGEADRSTLKK ALAHT\DHIQEAQSAWKDDFAL NSMLRRRFRVPSKP
3834	34202	A	3874	3	531	GRKRSKRMEKGERGEPYSLSLR NHQGSWEPEHMS*KPEGG\VLA FKGDDGFSVWESNAIATYVSNE ELWGSAPEAAAQAVQWVNFA DDSQYQGVPTLGKMHHDKQA TQDAGEEV/QPQFQAVLG\EMK LCENMAHFDAKIFAESQPKKDT PRKEKGSREEKQKPQAERKEEK KVATPAP

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3835	34203	A	3875	2	1326	TMAAGTLYTYPENWRAFKALI AAQYSGAQVRVLSAPPHFHFG QTNRTPEFLRKFPAGKVPAFEG DDGFCVFESNAIAYYVSNEELR GSTPEAAAQ\VVQWVSFADSDI VPPASTWVFPTLGIMHH\NKQA TENAKEEVRRILGLLDAYLKTR TFLVGERVTLADITVVCTLLWL YKQVLEPSFRQAFPNTT\RWFL TCINQPQFRA\VLGEVKLCEKM AQFDAKKFAETQPKKGTPRKE KGSREEKQKPQAERKEEKK\AA APAPEEEMDECEQALAA\EPKA KDPFAHLPKSTFVLDEFKRKYS NEDTLSVALP\YFWEHFDKDG WSL\WYSEYRFPEE\LTQPFMSC NLITGMLQRLDKLRKNAFASVI LFGTNNSSSISGVWVFRGQELA FPLSPDWQVDYESYTWRKLDP GREETQTLVREYFSWEGAFQH VGKAFNHGKIFK
3836	34204	C	3876	58	222	
3837	34205	A	3877	6	153	
3838	34206	A	3878	2	889	CPPWELILDQFRKSLGISPANTG PLCPAPPSCMYPPSPQMPAKAP/ PDHPPEGRPGTTPEPFPRVTCVT E/PVGKGLSRDSQ*ETRGDLQE* SLAAPKSAPCFTHSAICPGAPSM SRHPERSVFLLFQAPVQEPPAPG PP*WVLREPDFGTGVFPEPSW* KAADFEPLGLCPGRSLSAQCPS WWPPTSSDPG*ALLKSGTGTPT VAPRQPAPAAPRFQRPPQPRGL ASTCPAGPQQKGSDPPGRSAGS E/GSVSGKSLKPCLSSPLIPPPQS STQKKASVAKFVEFSPYTKQKS QLSVP
3839	34207	A	3879	1	391	MAKAVEKPESTLEATKSKESV MSRVEWIGTAHMWVDDETGD NASKTQQTLEPAELATKYANFS EGACKPGYASALMTAIFPRF\C KPIRLSP*PRHLAHWCKKWAPK ILGSSAPVALQGAAPVAALMG WR
3840	34208	A	3880	1	346	
3841	34209	A	3881	249	474	VYLLIVLAVLYTNNRQTESQIM SELPFTIASKRIKYLGIQL\TRDV KDLFKDNYIPLLKEI*EDTSKW KSIPCSWI
3842	34210	A	3882	25	302	
3843	34211	A	3883	1	2235	

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3844	34212	A	3884	1	2724	MGGMVESSRHNWSGLDKQSDI QNLNEERILALQLCGWIKKGTD VDVGPFLNSLVQEGEWERAAA VALFNLDIRRAIQILNEGASSEK GDLNLNVVAMALSGYTDEKNS LWREMCSTLRLQLNNPYLCVM FAFLTSETGSYDGVLYENKVAV RDRVAFACKFLSDTQLNRYIEK LTNEMKEAGNLEGILLTGLTKD GVDLMESYVDRTGDVQTASYC MLQGSPLDVLKDERVQYWIEN YRNLLDAWRFWHKRAEFDIHR SKLDPSSKPLAQVFVSCNFCGK SISYSCSAVPHQGRGFSQYGVS GSPTKSKVTSCPGCRKPLPRCA LCLINMGTPVSSCPDRSTRQKV NKDIQELNSALHQADLIDIYRTL HPKSTAYTFFSAPHHTFSKIDHI VGSKALLSKCKRTEIITNCLSDH SAIKLELRIKTFTPNRSTTWKLN NVLLNDYWVHNEMKAEIKMFF ETNENKDTTYQNLWDTFKAVF RGKFIALNAHEKIQTTIREYHK HLYANKLENLEEMDKFLDTYT LPRLNQEEVESLNRPITGSEIEAI LNSLPTKKSPGPDGFTAELYQR YKEELVPFLLKLFQSIEKEGILP NSFYEASIILIPKTGRDTTKKEN FRPISLMNIDAKILNKILANQIQ QHIKKLIHHDQVGFIPGMQGWF NIRKSINVIQHINRTKDKNHMII SIDAEKAFDKIQQPFMLKTLNK
3845	34213	B	3885	1	1971	
3846	34214	A	3886	1	1146	METRPSRGPLTPHTARCQSETK LPEEGSGSNICCSAIFAILQPPLV IPRQTGSGVDLQQTPTDLELRD LTVRRKTNKWKGIASTSTKRTS TPKRHLSWFFEKINKIDRPLAKL IKKKREKNQIDTIKNDKGDITTN PTEIQTTIREYYKHLYANKLEN LEEMDKFLDTYTLTRLNQEEVE SLNIPITVSEIEAIIKSLPTKKSPG PDGFTAEFYQ\ASIILNGQKLEE FPLKTGTRQGCPLSPLLFNTVLE LLTRTIRQEKETKGI/QLGKEEV KLSLFADDMIVYLENPIVSALN LLKLISNFSKISGYKINVQKSHA FLETNNRQTESQIVSELPFTITTK RIKYLGIQLTRDLKDLFKENYK PLLNEIKEDTNKWKNILCS

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3847	34215	A	3887	66	1392	QVLLSFGTPLVLTTKREKNQID AIKNDKGDITTDPTEIQITSIEYY KHLYANKLENLEEMDKLLDTY TLPRLNQEGVESLNRPITGSEIE AIINSLRPISLMNIHAKILNKILG N*IQQHIKKLIHHDQVGFIPGMQ GWFNIRKSINVIEHINRTKDKN HMIILIDAEKAFDKIQQPFMLKT LNKLGIDGTYLKIIRAIYGKPTV NIILNRQKLEAFPLKTGTRQGCP LSPLLFNIVLEVLAKAIRQEKEI KGIQLGKEEVKLSLFADDMIVY LENPIISAQNLLKLTGNFSKVSG YKINVQKSQAFLYTNNRQTESQ IMSELPFTIASKRIKYLGIQLTRD VKDLVKENYKPLLKEIKEDTNK WKNIPCSWVGRINILKMAILPK VIYRFNAIPIKLPMTFFTELEKTT LKFIWNQKRACIAKSILSQKNK AGGITLPDFK
3848	34216	B	3888	1	2868	
3849	34217	A	3889	1	1218	
3850	34218	A	3890	1	1893	MKEIETQKTLQKINESRSWFFE KINKVDRPLARLIKKKREKNQI DAIKNDKRDVSTDPAVIQTTIRE YYKHLYANKLENLEEMDKFLD TYTLPRLNKEEVESLNRPITGSE IEAIINSLPIKKSPGPDGFTADFY QRYKQELVPFLLKLFQSIEKEGI LPGSVYEASIILIPKPGRDTTKK ENFRPISLTNIDAKILNKILANRI QQHIKKLIPHDQVGFIPRMQS\W LEVLARAIRQEKEIKG/IQLGKE EVKLSLFADDMIIYLENPIISAQ NLLKLISNFSKVSGYKINVQKS QAFLYINNRQKESQIMSELPFTI ASKRIKYLGIQLTRHVKEHFKE NYKPLVNKIKEDTNKWKNMPC SWVGRINIVKMTILPKIERIGKT KGTETQRGKSCKPTHPVSVISL AESIARDFCLQLNRARSCDQSS YNEVLEADNRAFSLCKGMPFD RLSPISQTPGPSWYQSSPYQPMF LAAPIDIGSRPASMDPIHSRTWH YVTVVILARSRKHQELILSESKQ FEEAPPELRSRAPGGFSKPAAG QIKVGLRENLTASMQISPADAN LILQDSFLAIFLFQALIVTIYKEN EKEEGQERREEALRSTGKNNV WKNTDIDRPESISDSESAGCDY

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3851	34219	A	3891	2	1562	WGEIRAEKLKIPKTGAPLFLQRI AAPRQQRNKTGQRMSLTS*QK *ASEGR**QT/LSKLKEHVLTHC KEVKNLEKRALAKLIKKKREK NQIDAIKNDKRDITTDPTEIQTTI REYYKHLYANKLETLEEMDKF LDTYTLPRLNQEEVESLNRPITG SEIEEIINSLPTKKSPGPDGFTAE FYQRYKEEL/PDKQLQQSLRIQ NQCAKITSIPIHQ*QTNREPNHE *TPIPNYYKENEIPRNPTYKGCE GPLQGELQTTAQR\KRGHKQM EEHSMLMDRKKQYCENGHTA QGSTDFGEVQRLRLWQEDDVA EEVSGFFEEDNLKSVAQDPFWE SRQVKTIFNCVDTYIAGAKAIA GITQVTCTGNQFAEINQRFLKL KKSWSLYRRFQPWQEECGPSW NPSWTHPSVASSRKDAAAQRE AQEGDLQGQEGAEASHAGGPA ADHYSGTAHAGRGRALDRGVC VRGHAPPPITELSRPAGCGPHR QGEEAREGDANKKNGFHIQRC SCCLSCKQEHPVLPLVFGLD
3852	34220	A	3892	2428	6109	YPESTMNSNKFTRKKSNNPIKK CQQASQLKALPTQSCSPSSNSY ETFLVSPLHPFQFYISFPHYTEM VPPLTPEDYNSRGDFGGDTETN HIISKFHRSLEQVQNAASRRSQ DGRIGTAPVYSSQRERRRRRVIS AFPSEERSSSPAMEQSWMENDF EELREEGFRRSNYSELREDIQTK GKEVENFEQNLEECITRITNTEK CLKELMELKTKARELREECRSL RSRCDQLEERISVMEDEMNEM KREGKFREKR
3853	34221	C	3893	13	391	
3854	34222	A	3894	117	704	WLSAWPRACPDCRVRFPHTSPP CLPCGPEAEPGPGPALRELVQP LPGQLQPPFGMPLPLVPAGSFLI CTVWERPRPGLAVGSPPCFPSL H/PTVPVGCPPPSPCL\RPPA*PT THLHIWPSLLFGPLPALPPPLAA SASAGLRKPWLDGLHPSVEPSG LGAAPSPAPPACAWTRPPHLHP SSFSSCVPQISSLFLCF

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3855	34223	A	3895	1	1185	SAASSVLYVHNEPQVHGAHQK IHPIHPSLHYCLAHIISQDLHTS MNALGLFGVG*EQGLQEKSNL SSTHHEPGHGGQDAAGARDGA RGRGGS\TGSAAGERGGRTVPH WA/GQPAEAGGAG*PRGPQLRR SPPP/RLPPRAGSSANTRNSVLL* FF*AVCLWADHYPL*TLISSS*M AGRWRSVPGIPTSPTK/PPPPPPP PPPPPPPPPPGSFLSEP\VWSTA* NSTCPPRRCRSASGGPIWCPCRP /PAPPPAPPAPPPLEATEESLEEG \GGRASRSANMFAPTAPAGSSW HRARWG*PAWKAGAAGTRGA KCGQFVPSASSAP*LAGGWPGA GGQRGARRAQKAWCCRPGTSL /APGPELFPESALVQAGSAPPPP PPPPPPPLCLLLLRAESEGAVLM
3856	34224	A	3896	192	477	
3857	34225	A	3897	2	1782	RAAARKEHQGSAT/RAERA/PR TPKAS\GRG\SPVPTSGTVTART GTAPRGLSAEDGRRRGRP\IGIP FTDHSSDILSGLNEQRTQGLLC DVVILVEGREFP\THRSVLAACS QYFKKLFTSGAVVDQQNVYEI DFVSAEALTALMDFAYTATLT VSTANVGDILSAARLLEIPAVSH VCADLLDRQILAADAGADAGQ LDLVDQIDQRNLLRAKEYLEF/ YYQSNPMNSLPPAAAAAAASF PWSAFGASDDDLDATKEAVAA A\VAAVAAGDCNGLDFYGPGP PAE\RPPTGDG\DEGDSNPGLWP ERDEDAPTGGLFPPPVAPPAAT QNGHYGRGGEEEAASLSEAAP EPGDSPGFLSGAAEGEDGDGPD VDGLAASTLLQQ/MDVIGGPGG G\RGGGQRRGVAGRRQGRHGL LPEVLQRRPRRRRLPGLVAEGG EEDPSQGLPEVPHLREGHPGRR QAAATHPHPHGREALRVQHLQ GPLHQDTSTSTLQKPGSPRPL*V TAGR*AGQAEGAHAEAHGREA VPVPAVRRRLCPQLRPEEPHAR AHGPAPLPVRQLLQDLRPLRPP AQTPQERRLQRRPLAPAVPASP CVLWAGGCPDPQPW
3858	34226	C	3898	162	356	

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3859	34227	A	3899	3	2289	GELHGVAEQAEGDPREGSPGP AEQASGTELREVPGPHWPLHPP EAPVCQHYHRPMVQKGN*GSV WGRGESLVQG/AHGQTSQRSV QMTGGGAWTGQTSQRSVQMT GGGGTPRGSRSSSPRTT\TPGTA EDTEGEPAGAGEQAAGRPVRP LHGHPGAGQEAAAGVRELPPA EPAAHLHPQPALLIQQHPISHAR SQHPRRPCCLPGPGLRAGGTAE GLPCAFCSQRDERAEGRERDLE GGGEAASGPGRQAQAPGQGGH LGPPLTPAAPLPWWLEGHHRE ATGRPRGG*GRPPGRGPTGRRK ASRAQDISSGQNLPRGHPA*VA SPRHEPPAHLQPAARDHCRGA\ PGSQACPADRGPANGTPPPLPA RSSPPSP\GMSVASPWTASCGPP GPPP*P\IGPEALPEGGPALPPKP PPVPAPSEPPQQPPGPCCSPQRP PAPGPEGQRSRGLGGAHRTAG AAQCPGGHAGPSPGGGTAPAP GPAAAAG*GQGRQCQAKGPAH TRGDAALPTSRLRL*GP*E*GD QGSSG\AAGLSGGRHTQPAGPG RAQRTEAAATQDCALDKPLDL SEWGRARGQDTPKPAGQHGSL SPAAAHTASPEPPTQSGPLTRSP QALSNGTKGTRVPEQEEASTPM PPDLDGHP\GPARLKC*DQSPTN WMRQTPQAA\SGPELPGGG\PT STTGEGPECICTQEHGQGPPRK
3860	34228	A	3900	3	3169	ASQLVLTLAYQANCVSVSYTD LLGKPGGSYFTFLYVLNIRSRSR LKKDYDDFRRQPDHDTFNREL WTTDEGEGDLGKDSPKGEISKS IDSTEPLDILEKDHFDSDDMKLS EIDFPMARSKLLKKELPSKDLP KTLLKTLKRQSKQTDYVDDST KELSPRKKAKLSTNETTVENLE SDVQIDCFSESKHTEPSFPESFA SLDSVPVSTLQKGTKPIQALLA KNIGNKVTLTNQLPPSTGRNAL AVEKPVLSPPEAS

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3861	34229	A	3901	33	1227	HHLRGTGQRAGQQLPPGMKM GRAGPPGPWCEHTT/PPSRGRPT SSGGPTLAPALAELSPRPQTPSP SISSLPMITSLPGGTGPLCLRPLS WEKPGSATGK\RGSQQEVDVG PSPGHTAPSKSHGQGPVGSPSA RQGCGPASSALQRRREPGGGPR GHPAGPHGGCVLPPWPGCPGN TMQRL*GFHTRAMNTQSGAGP RTAPSPRAQGAQGRPSKSCSGA SQGPCPAVGPH*APGEDRVRHP LASISGTTRAHGRPSQQREPRN KSTRADSRSPRTVPPHGPPGPSL PRGR\PAQPGPGV*RNGISVGAG RFPPFTAPCGQQARPGAG\NRG AGSGA\PEL*GGLGRDPGSSGCE VPGGRAGG/PPRT*HFLARPAPP SPPQGLPRPPKVLGLQA*ASAPS
3862	34230	A	3902	124	1183	DNRAVFSPTGRR\DRGGGGPAG TLARV*SAPGAFGV*STRTHVA GVQMPPVPGTCDVCTRPCSPVS RPPRASTAVAAAAS/SGPRQPR HPRHTSPMPPPAALRPPAGPRG LAPGG/HTAPPATAAPVELQHP LLRLQTGPPLGPPTGPA*EPRAH PCIRGLLPAGSGPPPRRQGHPEP PRLHTAACSPCQPQRALESSCPP RAFPGTAAHWLLGTGDWLL*P AAQAALASQEWALPGICLCNSL SEPTGRVILASQLAPCIRLGCRK RSLAKAPKLISGGAGAHTPTPE PTCFSVSVLGTSPPAAGGPRGQ ESVVSSPVTMGT/VPAWAIPSLG CRGEASLDHPAGQLPARGQRSR RH

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3863	34231	A	3903	174	1599	VLHAVGNQVQGCPGPEVHVCG WRPGCVRLLQLHVVGRADGPE CDLCAVWPGGGDV*PAVPGAV PHVTQCEPQGHPYGEGTGAGA YCAALCGPPGARGHCGQEARQ PQVRTCQGQERRRDCQDLL*E AGGQEAPGAERPSAG*ASRGTP RAAATHPPRTASPGEGQHV*VP AHVGGARPGAWQRHPGLHQY HRPQHLEPPAQPDEPHQDP*HL PGQRPAPAVEAEPGQQAPS\KP CPPPEPSAPQDGVPAENGLPQG DP/GAIAPRAQAPDSPCGRCTSP GQQ*YWLGPGAPQRGSSPEWD RP*ATQDGRPRPRPTPAAAICDP G*PREPRGGAPQWAGWGGRRR **RLRNPQ*PGQP\SGSSGRGPG PRRPSVASSVSE/RVLRGERALS PSPEAPLRASGQRANPTTAPAA ECPPYNPRDLCWTPGWLPMGP ESGKRRSRCVEEDAGPALHRQ GGTDGET**TGRGGNRPGPYGR
3864	34232	A	3904	331	1120	HKDRFWQLQNDSCFLHSPGER QWLGGPRSDTFGPQVLFGHVGI CSQRA/HPAGPGHRGLPEGR*PP HRSQRHPPRSRKPYLA*PPDMC VATDRRTQTPRDFPPLGR*KPH GTLRSAACPAGRVSPSPRPRGL PAPPPKSHLCG\PGVRGR*QLLP PHPGSPKGERGWTASPGAARG GPGPAPAPRP\RASWSQPSVTFP LPLAGLA/GHPGSRTEPAWKAG GAAARPGPELPRDLLQAGSTDT ASGEQLAAGPWTGKEISGRARP RL
3865	34233	A	3905	2	415	YTILTEK*KLSKLST*W\VHQDQ LQKREELSMEILNK*DQDSEAY PQRTVTGEETWLYQYDPPPLPR SLPPPQTHTAPVGA*S/DWGG*E LPPGLNGDKLAHHSPTPFLSFSG LLFVDWL*SQLLSLFGLFTQGVI RIFI

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3866	34234	A	3906	1	4527	MGFCCRECRPRLLKGRPCIQHA GPVAAFKVATPYSLYVCPEGQ NVTLTCRLLGPVDKGHDVTFY KTWYRSSRGEVQTCSERRPIRN LTFQDLHLHHGGHQAANTSHD LAQRHGLESASDHHGNFSITMR NLTLLDSGLYCCLVVEIRHHHS EHRVHGAMELQVQTGKDAPSN CVVYPSSSQDSESNHGNNFRIH VSNGLLMRGPRPLDRERNSSHV LIVEAYNHDLGPMRSSVRMRK LRQSTALAQHWTGTALDR
3867	34235	A	3907	1	2180	MALTFPCRKFEWYGRRQPEVR YSVPASHQLKATDADEGEFGR VWYRILHGNHGNNFRIHVSNG LLMRGPRPLDRERNSSHVLIVE AYNHDLGPMRSSVRMRKLRQS TAL\DSTGQAQHWTESRSGSPG SPVAPTCSART*QTSAS\VHLCL SGKSHHAWPP*TPFKLYYVH\E YSAHIHKENLVLVIVYVEDIND EAPVFTQQQYSRLGLRETAGIG TSVIVVQATDRDSGDGGLVNY RILSGAEGKFEIDESTGLIITVNY LDYETKTSYMMNVSATDQAPP FNQGFCSVYITLLNELDEAVQF SNASYEAAILENLALGTEIVRV QAYSIDNLNQITYRFDAYTSTQ AKALFKIDAITRILGTQMDTKM NKTLLSPQRVLRLEVEMELIQD ANQSATRRCAENYNRGVVEPL RAQQSYLAGEAGRLHGRGGFP VECEREEGIQQTECPGEVMPDR GSDMEGVITVQGLVDREKGDF YTLTVVADDGGPKVDSTVVSG TRVYITVLDENDNSPRFDFTSDS AVSIPEDCPVGQRVATVKAWD PDAGSNGQVVFSLASGNIAGAF EIVTTNDSIGEVFVARPLDREEL DHYILQVVASDRGTPPRKKDHI LQVTILDINDNPPVIESPFGYNV SVNENVGGGTAVVQVRATDRD IGINSVLSYYITEGNKDMTFRM DRISGEIATRPAPPDRERQSFYH

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3868	34236	A	3908	603	1395	RGRPRGSPIFPTRAPREKKR*EE VGGHKREQTG*GGGERRKPPN PQHEPKERGWCSRVPEEPQ/RK RRSARARPKKL*REKRRRGRPK RCLW*TGRHPSHHPRTHQC*F* WRK/REEGKERKKEQPAHAGQ KRRKAARHRRRRRRRERTDEK NRTWTRRRREKAGQDEKREGE HGQKRSQQGRESRRDGRARTR KERRQKRENDNRARRRQQAER EKTKSVKRRQTTQQAEEVRQA RENEAREPQQRRQHSRRRKEKE EMRAPRSKQ
3869	34237	A	3909	1	548	
3870	34238	A	3910	1	1803	
3871	34239	A	3911	1	279	
3872	34240	A	3912	1	506	MCYSRQSNLGTFGEGKIKGSEV IDECPRSSRYQDLQELQNKTKL TVLEGDILDESCLKRACQDMSV IIHTTSIIDIIGVTHRESIMNINVK RTQLLLEACVQATVPVFIYTSTP EVAGPNSYKEIIQNSHEEEPLEN T\WCSPS/PYKKA/LARSGI*ATL QLGGSQEECT
3873	34241	A	3913	3	621	AGQQTVEIDLRHRIQLP\DLENQ RNFNELSRIVLEVRERVRQEQQ EGGHEAGEGRGRQGPRESQPSP AQPRAEAPSKGPDGTPGEDGGE PGDAVAAAEQPAQCGQGQPFV LPVGVSSRNEDYPRTCRMWNS TFQTYKKEVCLPRHSMHPGPW AICCECQTRFGGRLPVSRVEAA LPYWVPLSLRPRKQHPCWMHA AGTTAGGSAVMS
3874	34242	A	3914	1	430	RHRIQLPDLENQRNFNELSRIVL EVRERVRQEQQEGGHEAGEGR GRQGPRESQPSPAQPRAEAPSK GPDGTPGEDGGEPGN\AVAAAE QPAQCGQGQPFVLPVGVSSRNE DYPRTCRMW*GCGGYWGLKV GQHGLQRGPQPHT
3875	34243	A	3915	2	1175	
3876	34244	A	3916	1	256	HLRIHTQESSYVCDECGKALTS KRNLHQHQRIHTGEKPYECSKY \G*PFGLLPQLGHLEHVYSGEKP VLDICRFGLPEFFTPFYW

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3877	34245	A	3917	1	1396	MRPQLAGRDHHRGAATLLLER PGRLVTHFRQRRGAVRYGGGK STTQHLSQRRLSGPNDHTKGLV WLLEHILQRLVSFVKLQATRTF TRTYITYAWFLPWGFSGVLCGT PVDTCWALKHQRIHTGEKPFEC SECGKAFNGNSSLIRHQRIHTGE RPYQCEECGRAFNDNANLIRHQ RIHSGDRPYYCTECGNSFTSSSE FVIHQRIHTGEKPYECNECGKA FVGNSPLLRHQKIHTGEKPYEC NECGKSFGRTSHLSQHQRIHTG EKPYSCKVCGQAFNFHTKLTR HQRIHSEEKPF*L/CVDCGKAFS AQEQLKRHLRIHTQESSYVCDE CGKALTSKRNLHQHQRIHTGE KPYECSKYEKAFGTSSQLGHLE HVYSGEKPVLDICRFGLPEFFTP FYWKEEKKCGRKMRNEVVHK VSFFLVVPIALSSLLKKKWKML KKEKAQDPTEYGNLEDDNSQQ
3878	34246	A	3918	1	547	MDSQRPRER/QRERERQSERQR HTQRMHREAETEDERDWKGH DTKTRRQRQRKRAEEGQCREH DRERRRD\RTGERREKQRKSTQ QSRKPSEEPHREKTQIKRERGPE QGELERGQCTERNRKA/GTPEC *TDPHIWTPHPARSAPAHPPDH TAAKYRPPYRSHHSGITHQHPR AASTLKLWPKP
3879	34247	A	3919	1	399	
3880	34248	A	3920	3	872	KSKLKSEQDGISKTHKLLRRTC SSTVKTDDVCVTKSHRTFGRSL SSDPRAEQAMTAIKSHKLLNRP CPAAVKSEECLTLKSHRLLTRS WSGDPRCEHNTNLKPHKLLSRS YSSNLRMEELYGLKNHKLLSKS YSSAPKSSKT*/VFSKEP*RRRG RKALSLPQGLFGYP*HHLHPSSS QLAPNGAKCIPVRDRGFLVQTI EFAEQRIPVLNEYCEVCDEPHV FQNGPMLRRGRDVCEWAKKY ANSVVRKKFCRLSIARRSRYRA DMDLLRMSNFILTIIYKQKLNL
3881	34249	A	3921	3	218	CCRSHQGAGEGGHLSVQLLWQ YRWMWCSWGPV\FQFHTDLEL VAWRCVGLDPGCQQLDIGMQT LIGDHICVF
3882	34250	A	3922	1	1055	

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3883	34251	A	3923	3	962	RSMRQKVNKDIQDLISALPQAD LIDIYRTLHPKSTEYTFFSAPHR TYFKIDHIVGSKALLSKCKRTEI TTNCLSDHSAIKLELRIKKLTQN RTTTWKLNNLLLNDYWVHNE MKAEIKMLFETNENK/DETYQN LWDTFKA/PSIILNGQKLEAFPL KTGTREGYLLLPLLFNIVLEVL AMAIRQEKE/IKGFQLGKEEVK LSLFADDMIVYLEDPIISAANLL RLISNFSKVSGYKINVQKSQTFL YTNNRQTESQIMSELPFTIATKR IKYLGIQLTRDVKDLLKENYKP LFNEIKEDTNKWKNIPCSWIGRI KIVKMAILPK
3884	34252	A	3924	1	1452	MGDFNTPLSTLDRSMRQKVNK DTQELNSALHQADLIDIYRTLH PKSKEYTFFSALHHTYSKIDRT VGSKALLSKCKRTEIITNSLSDH RAIKLELRIKKLTQNRSTTWKL NNLLLNDYWVHNEMKAEIKM FFETNENKDTTYQNLWDTFKA VCRGKFIALNAHNRKQERSKID TLTSQLKELEKQEQTQSKASRR QEITKIRAELMEIETQKTLQKSN ESRSWFFERINKIDRPLARLIKK KREKNQIDVIKNDKGDITTDPT EIQTTIREYYKHLYANKLENLE EMDKFLDTYTLPRLNQEEVESL NRPITGSEIVAIINSLPTKKSPGP DGFTVEFY/QEGN*AGEGNKGY SIRKRRSQIVPVWR*HDCISRKP HRLRPKSP*AGKQLQQSLRIQN QCTKITSIFIHQ*QANRKSNHE* TPIHNCFKENKIPRNPPYKGCEG PLQGELQTTAQ*NKRGYKQME EHSMLMGRKNQYRENGHTAQ

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3885	34253	A	3925	1	1251	MKAEINMFFETNENKYTVYQN LWDTFKAVCRGKFIALNAHKR KQERSAMNTLTSQLKELEKQE KTNSKANRKQETTKIRAELKEI ETQKTHQKINESRSLFFEKTNKI DRPLARLVKKKREKNQIDAIKN DTGDITTDPTEIQTTIREYYKCL YANKLEYLEEMDKFLDTYTLQ RLNQEKVESLHRPITGSEIEAIIN SLPT/KKSPGPDRFTAQFYQRY\ DGMYLKIIRAIYDKPTANIMLN GQKLEAFPLKTGTRQGCPLSRL LFNIVLEVLARAVRQEKEINGIH LGKQEVKLSLFADGMIVYLENP IVSAQNLLKLISKFSKVSGYKIN VQKSQAFLYTNNRQTESQIMSE LPFTITTKRIKYLGIQLARDVKD LFKENYKPLLNKIKEDPNKWK NIPCSWIGRINIMKMAILPK
3886	34254	A	3926	1	1203	
3887	34255	A	3927	1	1233	
3888	34256	A	3928	1	951	MKREKNQIDAIKNDKGDITTDP TEIQTTIREYYKPLYTNKLENLE EMDKFPDTYTLPRLNQEEVESL NRPITGFEIEA/INSLPTK*SPGAE GFTAEFYQSVGSSGQGNQARE RNKGYSTRKRGTQIVPVCRWH DCIFRKLHGLSPKSP*ADKQLQ QSLRIQNQCAKITSIPIHQ*QTYR EPNHE*TPIHNCYKENKIPRNTT YKGCERPFQGELQTTAQ*NKRR HKQMEEHSMLMDRKNQYREN GHTAQGHL*IQCHPHQATNYFL HRIGKNYFKLHMEPNKSLHSQ DNPKQKEQSWRHHAT*LQTILQ GYSHQNSI
3889	34257	A	3929	1	814	

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3890	34258	A	3930	1	1545	HQLKVQFRIIISIRSSCDGSAWG VAPTFKTRGARSRSRAAIRLGA ADLDEVKSSLVNESENQSSSSD SEAERRPQPVRDTFQKPRDYFA EVRRPQDSAFFKGPPYPGYPFL MIPDLSSPYLSNGPLSPGGARTN SSPAPKETWICARFGGVSLSFLE IGSRVLLLGRDVNRSSSLLPAQI PIACHFAVDGGNFIRGKGAYLL TFDLFGNWGLFFLIEIAVWELS AHSSGQSEDALELSRGTCSSSL QLCWTAKALVGKGLDGGPVC KNSGICSTRTKTQEQMSFMEAL YQEGFLRETVVQAVRKVPQTP RKAVLEVLARAISQEKEIKGIQL GKEEVKLSLFADDMTVYLENPI VSAQNLLKLISNFSKVSGYKIN VQKSQAFPYTNNRQTESQIMSE LPFTITTKRIKYLGIQFTKDVKG LFKENYKPLLNEIKEDTNKWK NIPCSWIGRINIVKMAILPKVIY RFNAIPIKLPLTFFTELEKTTLNF IWNQKSR\IGKKILSKKNKAGGI
3891	34259	A	3931	693	1464	ARAEVKLSLFADDMIVYLENPII *ARAEVKLSLFADDMIVYLENP IISAQNLLKLISKFSKVSRYKINV QKSQAFLYTNNRQTESQIMSEL PFTIATKRIKYLGIQLTRDVKDL FKENYKPLLNEIKEDTNKWKNI PCSWIGRINIVKMAILPKVIYRF SAIPIKLPMTFFTELEKKNWLAI CRKLKLDFFFIPYTKINSRWIKD LNVRPKTMKTLEESLGNTIQDI GIGKDFMTKTPKAMATK/DQKS FCTAKETTIRVNRQPTEWEKIF AIYPSDKGLIS

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3892	34260	A	3932	211	2519	ENRKSNCLCLQMA*LYI*KIPSS QPKISLS**ANLAKSQDTKSMC KNHKHSYTLITDKQRAKS*VNS HSQLLQRE*NT*ESNLQGM*RT SSRRTTNHCSTK*KRTQTNGRT FHAHG*EESIS*KWPYCPSKC/K RTEIITNSPSDHSTNKLELRIKKL TQNHTITWKLNNLLLNDSWVN NEIKAEIKKFFETNENKKTTYQ NLWDTAKAVLRGKFIALNAHI GNLERSKIYTLISQLKEPERQEQ TNPKASRRQEITKIRAELKEIET QKTLQKINESRSWFFENIKIDRQ LARLIKKKREKNQIDTITNNKG DITTDPIEIQTTIREYYKYLYAN KLENLEEMDKFLDTYTLPRLNQ EEVESLNTPITGSEIKAIINSLPT KRSPGPDRSTAE/FYHRYKEEL VLFLLKLFQSTEKEG\GRDTTK KENFRPISLMNIDAKILNKILAN RIQQHIKKLIYHDQVGFIPGMQ GWFNICKSINVIFQYTNNRQTES QIMSELPFTIASKRIKYLGIQLTR DVKDLFKENYKPVLNEIRGHK QMEEHSMLMDRKNQYCENGH TAQGNL*IQCHPHQATNDFLHR IGKEEVKLSLFADDMIVYLENPI ISAQNLLKLISNFSKVSAYKINV QKSQAFRYTNNRQTESQIMSEL PFTIASKRIKYLGIQLTRDVKDL FKENYRPLLNEIKEDTNKWKNI PCSWVGRINIVIMAILSKVIYRF
3893	34261	A	3933	2	1304	
3894	34262	B	3934	141	2008	

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3895	34263	A	3935	1	1845	MVISVDAEKTFNKIQQPFTLKT LNKLGIDGSYLKIIRAIYDQPTA NIILNGQKLEAFPLKTGRRQGC PLSPLLFNIVLEVLARAIRQEEEI KGIQLGKEEVKLSLFADEMIVY LENPIVSVQNLLKPIRNFSKVLG YKINVQKSQAFLYTINRHTESQI MSELPFTIATKRMKYLGIQVTR YVKDLFKENYKPLLNEVKEDT NKWKNIPCPWIGRIN\ILKMAIL P/KELEKTTLKFIWNQKRACIAK SILSKKNKAGGITLPDFKLYYK ATVTKTAWYWYQNRDIDQWN RTEPSDIIPHIYNHLIFDKPDKNK KWGMGSLFNKWCWENWLAIC RKLKLDPFLTPYTKINSRWIKD LNVRPKTIKTLEENLGNTIQDID MGKDFMSKTPKAMATKAKIDK WDLTKLRSFCTAKETTIRVNRQ PKEWEKIFAIYSSDKGLISRIYK ELNFTRK\NNPIKKWAKDMNR YF*KEDIYAANRHMKKCSSSLA IREMQIKTTMR/YHLTPVRMAII KKSGNNRTRENYFKIHMESKKS QNSQGNRKEKEQSWRHHATRL QTIVQGYTVAKTACYWYKNRP TDQSNRTENQEIRLHTYNHLIF DKPDKSNGETTPYSINGARITG
3896	34264	A	3936	1	700	
3897	34265	A	3937	1	3489	MKSGHPEKEQDNSDVQETREIT IRGLLCTALMRHSTGAIAYLGV LSGSASLKLAGVPLRCCEGDKD AGHPLETQTALCERGRGARSLV GNTIMTSQPVPNETIIVLPSNVIN FSQAEKPEPTNQGQDSLKKHLH AEIKVIGVNLIQNVLERGWGKC QEMIYVLGLDICRPFFVSRVSEE GRMGQRGEEDANSLDFPPASLL CLICQEQGVNGESCSPVGMYH REIVPVYEVLSVITGLQIQVFSG KEADSVIKRS

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3898	34266	A	3938	120	1331	TSLGPIYCAVRHTSSCRKVGSSR CQHGCQLSVRLQLDQAHHKQL PWLAPKNAVVPKSLEDPQGRK EGVTALTPEAPRSGPPKRLQLFP PSLCPNCSKQGAYFSPFGVTAT LLATPFSRSRVLVLQPGRMRYA DKWRVSKMKRCCIEQWNSSEK THSARASHSLQRQRGGPRVGGS SLQAGCHVISAALSKEEALEWV ASFCRQIVQSYLRPLLCSGADP GAFMDLRGEELRSLELSLSYTP PSNEFKISMKLEAQDPRNTTST CIATVVGLTGARLRLRLDGSDN KNDFWRLVDSAEIQPIGNCEKN GGMLQPPLGDSFHCDVRVSILD LFCFLLSELPFTIDTKRIKYLGIQ LTKDVKDLFKENYKPLLNE/IK/ EDTNKWKNIPRSRIG*INIVKMA ILPKDFG
3899	34267	A	3939	1	1421	MDSMSGGGQYRKINGNPTSVK CPLLLLPAILTPEPVNRWRQSC KAFARHSPLAFRVTISTSTFFDG LLVTGLYTSTSVQASQSIGGSSA FGFVLEVLARAIRQEKEIKGIQL GKEEIKLSLFAGDMIVYLENPIV SAQNLLKLISNFSKVSGYKINV QKSQAFLYTNNRQTESQIMSEL PFTIASKRIKYLGIQLTRDVKDL FK\ENYKPLLKEIKEDTNKWKN IPCSWVGRINIVKMAILPKNWK KLKFIWNQKRAHIAKSILSQKN KAGGITLPDFKLYYEATVTKTA WYWYRNRDIDQWNTTEPSEIM PHIYNYLIFDKPEKNKKWGKDS LFNKWCWESWLAICRKLKLDP FLTPYTKINSRWIKDLNVRPKTI KTLEENLGITIQDIGMGKDFMS KTPKAMATKAKIDKWDLIKLK SFCTAKETTIRVNRQTTKWEKI FATYSSDKGLISRICNELKQIYK KKTNNPIKK

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3900	34268	A	3940	3	1566	IQTTIGEYYKHLYTNKLENLEE MDKFLDTYTLPRLNQEEGESLK RPMAGSEIEAIINSLPTKNSPGP DRFTAEFYQRYKEELLISNFSK VS/VIQNQWEKITSIPIHQ*QTNR EPNHE*TPIHNCFKENKI\LGIQL TRDVKDLFKENYKPLLSEIKED TNKWKNIPCSWIGRTNIVKMAI LPKDKTSKYIDVDENEGSHCGK RKYKYGMEKALEILARAIRQEK EIKGIQLGKEEVKLSLFADDMI VHLENPIISAQNLLKLISNFSKV SGHKINVQKSQTFLYTNNRQTE SQIMSGLPFKIATKRIKYLGIQL TRDVRDLFKENYKPLLNETKED TNKWKKNILSSWIGRINIVKMA ILPKVIYRFNAILINLPMTFFTEL EKTTLKFIWNQKRACIAKTILSQ RNKAGGITLRDFKPYYKATETK TASEMKYYLENKIPFKVLHMV YNVPTHPPFIGDLHPNTKVVSL PPNITSLIEPMNQGVISAFKDCY LRKTFVQAVATPEGETEMTVM QFWKDYNT

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3901	34269	A	3941	1	2580	MVKGSIQQEELTILNRYAPNTG APRSIKQVLSDLQRDLDSHTIIM GDFNTPLSTLDRSTRQKVSKDI QELNSVLHQADLIDIYRTLHPK STECTFFSAPHRTYSKIDHIVGS KALLSKYKRTEIITNCCSDHSAT KLELRINKLTQNRSTTWKLNNL LLNDYWVHNEMKAQIKMFFET NENKDTAYQNLWDTFKAMCR GKFIALNAHKRKQERSKIDTLT SRLKELEKQEQTLHSKDSRRQE INAEKAFDKIQQPFMLKTLNTL DIDETYLKIIRAIYDKPTVNIILN GQKLEVFPLKTGTRQGCRLSPL LFNIMLEVLARAIRQEKEIKGIQ LGKEEVKLSLFADDMIVYLENP IISAQNLLKLISNFSKVSGYKIN VQESQAFLYTNNRQTESQIMSE LP\FTIASKRIKYLGIQLTRDVKD LFKENYKPLLKEIKEDTNKWK NIP\CSWVGRINIVKMAILPKVI YRFNAISNKLPMTFFTELEKTTL K\FI*KQKRACIAKSILSQKNKA GGITLPDFKLY\YYKAIVTKTA WYWYQNRDIDQWNRTEPSEIIP HIYNHLIFDKPDKNKKWGNDS LFNKRCWENWLAICRKLKLDP FLTPYTKINS\RWIKDLHVRPKT IKTLEENLGNTIQDIGMGKDFM TKTPKAMATKS\KIDKWDLIKL KSFCTAKETT\IRVNRQPTEWK KIFTIYPSDKGLISRIYKEPKQIY

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3902	34270	A	3943	5	2130	QRLRRQHRLEQKTRSTTCHMR QSTTRSAERADTRIESMPT*TTP *HTDDVP/SHCTNSTHTATTSPS THNHQQTLTRVANVAQIRRTDI SSIAATEWISTINTHNYACRTRA VSQRRYVSDFEKRERPTSNTPE PRFRLVVSTPTLVGTTQGTYQP PPARSRISIASHLLPPLSLLPSSL DLDGRSTLACSSSVSQFSGSRGS PSSYIVATTRVISDVDYDMTTY YNSTITPIS/PSARS*CQRSVHLL LSSHRTYRHPLVSRHTSQEHSL GGPLHRH*YNPVGSRAAAWAS KSALV/SVSLEALVVSALI*LVA TRQRLVGICRTTPIRARSSVVR* VTRYQPNQRAPLIHATYHLLDR GQHPQSMQTISHWTTPPCWCL VCGKKSSLPCCSTSSMSTRRNQ YDTLSLTTSWVL*SSIFWLAFIL LPRTSLPWPTVS*LAANA\SSGS TPVNSSFRT\SVRRSKLVVPANE IETPSFVVVTKFSRSASSYDCSIE YASTYAINITIVNSYVFA/PTHTT REHTISYALTSPGQPQNKTRIPE LQWAF*AVRPSTQ/PSTVIYHAP TSQAIASCALHSLLGCLLGSAT APLPPTWTTPPPPPQLRTT*STG SLPHPPSC*TRP*PLAPRN*PFTG MSSQHCIPT*PQLASHSIALRG/S RARPTTSQTSIAS/SHSHS*LSHV Q*RPLSDQRSPLDHHAHSSILYA RASRISCLRVCAV
3903	34271	A	3944	254	884	MTPNYTSRLFLHMGVLFYPFYR RLT*HIRTHINLKGWK/NRHFM QMDTKNAEKALDKIQHRFMIK TLSKISIQGTHF\KIIKAIYGKSTT NTILNGEKLKAFPLRTGIKQGCP LLPLPFNIVLELLARAIRQEKEIK GIQIGKEEVKLTLFADDMIIYLE NSKDSSRKLPELIKEFSKVSRYK VNLHKSIALLYTNSDQAENQIK NSTSFTI
3904	34272	B	3945	52	843	

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3905	34273	A	3946	1	831	MEMLYCLIAEAGHISSRMATNT ANSAGLKPTCVCVALPLPPGRS APHRSCSQAGRELPGQGPRYYR HLPQLSILHSIGEGQGCGFWSER SFKGYPERPAGAAGVCRLQGC GRRGRGAPFRTTDFSSRPRGAA ERADQGPRAGSPWPRTTSGAQ RGRAQGQGHTARRRGNSNPGP SRARQASRRRRPATSGPPRGSP RPDRPRRRSPFYRSSSRETSRPP EGPRRPRAPALSAPAPGQPARP RPREPVPCGAVFTARDRLRPPA ATSHAPFSAANPRR*HRPGGPG ARRLGDAQLSRRST/SGAPRCS QTRSR*PTCVCVALPLPPGRSAP HRSCSQAGRELPGQGPRYYRHL PQLSILHSIGEGQGCGFWSERSF KGYPERPAGAAGVCRLQGCGR RGRGAPFRTTDFSSRPRGAAER ADQGPRAGSPWPRTTSGAQRG RAQGQGHTARRRGNSNPGPSR ARQASRRRRPATSGPPRGSPRP DRPRRRSPFYRSSSRETSRPPEG PRRPRAPALSAPAPGQPARPRP REPVPCGAVFTARDRLRPPAAT SHAPFSAANPRR
3906	34274	B	3947	250	281	
3907	34275	A	3948	3	639	DHTCRLRQRLRLRVLVGPVPG AGPAG*KGCYGGRSANHHGAP ASCHLARSSCGPRLPGRYSAQQ PRARCAASGLCGWTAPAADPV PSEVLASQEVQLLCAGE*SGSC GPTHADLQPSPGGTGEDGAAR AKRDLPGSVGERAAAPASGRL RACPGRPAGAPGPRARPPGGTA ALAQPPRPQGAAARPPSGIGWP\ GNNGSAQSKGRALMEQAAG

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3908	34276	A	3949	161	2377	SLFHGKVCHFLHEPLPLVYLSL CTGYQLFKPSLISWLEEEEELST LPRVLQEWKMCLKTKGPALW QDNFCLKTLNGIQLARNQNGEE LYDCKQCEDVFCKHPCLKTNM STQNRGNTSECIQYAKDLLSLY NKTSTIRKVSVFSKHGKSFRL\F *MFRSRESVHKINPLK/CTDYGK AFIYQSYLEAHRKTQSGEKLNE WKQCGEAFTHSTSHAVNVETH IIKNPYECKECGKDFRYPTHLN NHMQTHIGIKPYKCKHCGKTFT VPSGFLEHVRTHTGEKPYGCKE CGKAFGTSAGLIEHIRCHAREK TFKCDHCGKAFISYPSLFGHLR VHNGEKPYEHKEYGKAFGTSS GVIEDRRSNTGQKRFDCDQCG KVFVSFSSLFAHLRTHTGEKPF KCYKCGKPFTSSACLRIHMRTH TEERLYQCKKCGKAFTKCSYLT KHLRTHAGEKPYECMKCGKAF TERSYLTKHLRRHSGEKPYECK KCGKAFTERSDLTKHLRRHTG DKPYEYKDCGKAFVVSSSLVD HLRTHTGYKPYKCNACEKAYS RSCVLTQHLKTHAAEKTSECN ACGNSFRNSMCFHDRLKTLTKI KPYKCKDCGKAFTCHSDLTNH VRIHTGEKPYKCKECGKAFRTS SGRIQHLRTHMGEKPFECDQCG KAFA\FSQLVLHI*KHTREKPCG CEECGKTFAVSSSLTEHVKIHR
3909	34277	A	3950	6	455	GLLHERQAEARCSICLDYLRHP MTTDCRHYI*SARIHQCW*ELQ DISPCPVCLQHCPDKNLKRNFQ LCHMTDIAKQLLTTARRKRKL QGEEPVCRKSDVALFCEKDPEL LCHQYRVSLDH*DH/SPMPIEQ AAAKHRKQFESYIEPLEKQV

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3910	34278	A	3951	2	1009	WNGHRMN*MQSSNGLEWN/QS SNGKEWNHRIESNGIIIAWN\Q WYQHQTEKNGIFEWNRRESSN GPEWNHVMEWNG/DNPWTRM QSSSNGIEWNHRMDSNGIIFQW NGNGNHRIGIEWNYDQ\SNEWI\ QWNQHQTEKNGIIKWNRRESS NGPEWNHLMEWN/ENNPWTR MQSSSNGIEWNRMESSNGLEW NNH*TESNGSVESSSDGNER/QS SSNGIAWNHHKMESNGINIKW NQMESWN/WN*MNRMELSSNG IEWNQHQTEKNGIIEWNRRESS NGPEWNHLMEWN/ENNPWTR MQSSS/NWNRMESSNGLEWNN/ QLNGIEWNHHRMEMNGIIIEW NRIELWN
3911	34279	A	3952	1	1494	MASLLGAPRLAGWASGAGALS RGWAIRPADTGGNLGPVPRVPL PPDPVLTARWAPGVNSGSQFSC HCQAPILEMGHKGSSPGLGDAE VRAITVQCIRPIDGPQQPPGGGS AGRRLTIPASTQEWAQLPVGRV LANVLTEGGDTGNQPIPQRSLC RPQPCSHAETWGEVEAQVPAQ SNREQPAAAPGCGPGRGETGA RPETTFSPRRAPPNPYDEEGVR WSLEFMLCGTDGPVQPVQHQE GPAARLQLIRGGSLILESEGTLR G/SPVLQTDQPASHLLHTQGFW A/AALSAVCL/HQNIIHSGSALL APATRAAWEQIQRSEGGTAQL LRRLEGYFSNVARNVQWTYLQ PFVIVTTNMILAVDIFDKFNFTG ARVPWFDAIHEAFPRELESSISF PANFFKPPEEKEGPLVRPASRK TTPQTTRPGPGTEREAPISR*KR HPDDTG*FTFTLGIVYCTPGQLP PEPYDPNRRSLWLPHWPIINTS MVSALVYSEGAPLPSPL
3912	34280	A	3953	1	681	MGQLLDKNTPSHGARTREECG RERLCVSPSQTGDTPRTSAYLC VGGPAWSPLSESRPAGSSGCPW IKPPDPRYSPIGLCSLLTTEMMS RQPRTDLRGQTNPAA\PSAPVPL SCSQNLPVWPSLMAGTTWHSP L\SPSCFWHSPGHN*H*CCVSKD *KSLFWEPTA/YSPLLPSTSP/SS KSMQPPKPRSNADSSVQASLIP RAMSSPTVSPWIMGNGSQGFD HIAVSMWDD

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3913	34281	A	3954	136	420	RESRNLSRGEESEDPAEPS\RNG *EHPLCYLQ*EFLQVLTMLQAE GTMHHFRSICQVNRNFLERGH/ SPPSPAPPPETHTGSPRPPSGRSR IRAYLH
3914	34282	A	3955	1	1782	
3915	34283	B	3956	1	3070	
3916	34284	A	3957	104	279	STTHPSVHE/QEEEEEEEEEEEE EEEEEEEEEEEEEEEEEERKKEC SKAQCKHFPLSEVL
3917	34285	A	3958	1	252	MTVCIHIASEDLPVGRDVEVED SDIHDRDPGLGDKSETPSE/EKK EEEEEEEEEEEEEEEEEEEEE EEEEEEEEEEEEEEEEEEEES NFLQHYLHL
3918	34286	A	3959	2	368	
3919	34287	A	3960	239	432	CLWLFQEEEEEEEEEEED*EEE EEE/EEEEEEEEEEEEEEEEEE EEEEEEEEEKIFLGHRVGI
3920	34288	A	3961	1	577	MQIPSLHKLKKEEEEEEEEEEE ERRRRIGRGREKKEEEEEEEEE EEEEEEEE\EKKKKEEKKKKEE EEEERRRKKKKERKEEEEEE/G KEEEEGEEGEEEEEEEEEERRK EEEEEEEEGEEEEEEEESCLMGP MCVHIHP\DKDLYSLGPPAQRF TGSHAELPT*KARRSSSWTAAS RGCAARDPPRRCSPA
3921	34289	A	3962	327	559	PKGRTPSPSCIHRYPCQTPRPHE P*GCHCPEEK/PRPRVWGPSRC MPLGSVQEKRPCPAPGGVQGSF RVSPLMMLTRL
3922	34290	A	3963	1	577	MQIPSLHKLKKEEEEEEEEEEE ERRRRIGRGREKKEEEEEEEEE EEEEEEEE\EKKKKEEKKKKEE EEEERRRKKKKERKEEEEEE/G KEEEEGEEGEEEEEEEEEERRK EEEEEEEEGEEEEEEEESCLMGP MCVHIHP\DKDLYSLGPPAQRF TGSHAELPT*KARRSSSWTAAS RGCAARDPPRRCSPA
3923	34291	A	3964	157	272	WCNGSPLYSGW*LVGMESLGR MHKDLWTRQPNQDQDLQ
3924	34292	B	3965	1	3723	
3925	34293	B	3966	1	573	

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3926	34294	A	3967	3	424	AGGQALQGPGQGRGSQGVVG/PGTGSSGAQHLGKHYPVLSGGSERSWGRSHTPAGAGC*VRGRRAGGRPGTGHSRPPGGSCLSPAPPNSARWLGLGAPWQAGAGLRDPGDWRRGQGGPGWAWCPGQPPAQPHTCPPNSTARY
3927	34295	A	3968	3	1238	RGAERRAWSRGPACTRRGPADWAAAGAGRPCPQRRGVCCTAAVPGAARLSCPTGPGPGDPGRRSLTGQGS*GLGAAFGGWTGALPSWHS*SQGWQTDPVR*VRGTERDICTGL*QPCPPGGLQTGSGGLEHSLPWPGIGIQAP*GPNHPCRLPRS*ALSAGG\SGGQALQGPGQGRGSQGVVG/PGTGSSGAQHHCCPPYTPPG*HPIPSLLALGPQSLQPEWAHSGTASGEQHSAGEHGMGTTGH*LPGLCSRCVLGKHYPVLSGGSERSWGRSHTPAGAGC*VRGRRAGGRPGTGHSRPPGGSCLSPAPPNSARWLGLGAPWQAGAGLRDPGDWRRGQGGPGWAWCPGQPPAQPHTCPPAGSLPGAAPGVLCAA*GPAAGV*AGPGPGPGSRR*TRGPSPGAPRPA
3928	34296	A	3969	3	415	ETGRHRSQQSVSSPPVQPRGKRAMYHSAAELVSRGFPRPPVQAPAEPAGAAEGVHSQPASRQEA/GS/TEVRGQAHRFVSPPNAAGAGDG/PDPQSLLAPTNRPCPPGGISPARSEPVPPAPGRAAP*CFPDLPGLAPPLC
3929	34297	B	3970	1	657	
3930	34298	A	3971	125	524	EAEALENQSQPCDTG/PQSAFSPPGSTQHPRSQLSQCKQRYQDLQEKLLLSEATVFAQANELEK*RVILS\GEPLLKQDSKQVQVDLQDLGYETCGQSKNEAEQEETTSPEHEEHSSRKEMVLVEGLCSEQG
3931	34299	A	3972	1	648	MGQVWGLVHFTLEVFHTGDEEEQEYSEVTEDVTEHVYLPAKAKVAKEEEAGIQQARQEGDLEAWQFPVRIHPPDQQENITATFEPFPFKLLKELKQAINQYGPGSPFVMGLLKNVTVSSQMIPTDGDPLTRACLTPAQFLQFKTWWADEASIQAARNAWAQPQINITADQLLGVGGWAGLDAQFVMQDDAIEQLRGVCIRAREK\IT*CGEQYPSF

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3932	34300	A	3973	350	1078	GSNRRSNRAEQLRGVCIRAWE K\ITSGEEQYPSFSIVKQGPREPY TDFIAWLQESLKKVIADSAAQD IVLWLLAFDNANPDCQAALRPI RGKAHLVDYIKACDGIRGPAG RLSWLSLQGRPAGAARCTSSSS DWKAQLAPGPHAGPLRCPAFR ARQPRLPAVLSAGAAFRDCPLS CVQALLGGSAGPGDRLPGHYS ALVALSLPFVKEATMNRWSRN HRSAFFLFSANAHGAEGVLSHT VASR
3933	34301	A	3974	2	630	WDNCGLWFIPSWNLFTLMMRR KESLMK*QKK*QSRFVCQLKLK /PAKEGEVYPYPSAPPPYFEEKE WPDPPDLSFLEDAGQKVIAPVT VQAAPQAIALSSIQAGIQQARR EGDLEAWQFPIRIHPPDQQGNII ATFEPFPFKLLKESKQAINQYG QGSPFVMELLKNVAVSSQMIPT DWDALAQACLTLTQFLQFKTL WADEVSIQAACNA
3934	34302	A	3975	264	634	WSSRCQHSSRPQASESWFPG*G PSFWPRIQGDEKTGAGGHP*LG C*PGMTGQGFSTKCQHTCLMW GSHWAQEAPENAPGTSCPGSSG SWVLRSSLQRQKSAWSPG/ASM PAPKMPFLTPSSGFS
3935	34303	A	3976	3	410	KKKVWREEKERLLKMTLEERR KEYLRDYIPLNSILSWKEEMKG QGPK*\EENTQETSQVKKSLTEK VSLYRGDI/L*VDAIVNAANASL LGGGGVDGCIHRAAGPCLLAE CRNLNGCDTGHAKITCGYDLP AKCEYN
3936	34304	A	3977	74	432	MLHNLRPRTLTTRTRCPSTPS*T TT*ATPPTTTHGSAGPRAAHLR RTGTRRWRAPRRARSCTRSSPR RARAASTPPLAPARELRSPASPP SCEQSAAPPSGRNGGNFPESIFV KTINSN

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3937	34305	A	3978	2	894	WGGYGMRTGPRTLTTRTRCPS TPS*TTT*ATPPTTTHGSAGPRA RTCAAQRTSGSHPSQRRTSSAA PGV*RANVFPWAH*MKRV*TT LENLTA/PEMAMPPAPHVIFAT DDWAAMVHPSARVPGLDGTG ALLVPTGVCAPGPCKCPLTSSS VTHTRLKTTLSVPPSARQTGRC RSPSDLRCSYPPDEQPVCVPKC GSPWVSVLVAWIQSESAVLDPR HPQHPYLYPVDMQNLLTNLGE PPQARALAAKLLGRPSSSQSGS RVPAVWAQAGNATYITVHTLC SHNTHMSPVRVKRFTHLG
3938	34306	A	3979	157	570	
3939	34307	A	3980	1	936	
3940	34308	B	3981	257	3934	
3941	34309	A	3982	210	4286	MPLKTRTALSDDPDSSTSTLGN MLELPGTSSSSTSQELPFCQPKK KSTPLKYEVGDLIWAKFKRRP WWPCRICSDPLINTHSKMKVSN RRPYRQYYVEAFGDPSERAWV AGKAIVMFEGRHQFEELPVLRR RGKQKEKGYRHKVPQKILSKW EASVGLAEQYDVPKGSKNRKCI PGSI\KLDSEEDMPFEDCTNDPE SEHDLLLNGCLKSLAFDSEHSA DEKEKPCA\KSRARKSSDNPKR T*L*KRATYNFEAH
3942	34310	C	3983	163	309	
3943	34311	A	3984	72	424	RNCGTARSQHEPLGSWLQDTP QPP*TLELAGNLPGD/F*PGPGK EQGMFVCHPIRQPLPRPLPGSSH QSMPTAQPPLSSSSALLPALPAG FPVTQGQWTKLQVQAPAPFHL PPQVEAV*AFYQKQMLVPCSL* SMPTAQPPLSSSSALLPALPAGF PVTQGQWTKLQVQAPAPFHLP PQVEAV
3944	34312	A	3985	1	347	KWQRFVLTGIDTYSRYEFAYPA CHASTKTTIHGLMEFLIHHHGIP HSIASDQGTHLMAKEVRQWAH AHGIHWSYHVPHHPEVAGLIER WNE\GLLKSQLQHQLVNRLRRE LQCWLG
3945	34313	A	3986	1	1716	

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3946	34314	A	3987	1	737	MSSVLLRLIYQLTQKTASFEGG PEQKALQQIQAAVQAALPLGPY DPANPMVLEVSVADRDTVWSL WQVPIGESQLGFWSKALPSSAD NYSPFERQLLACYWALVETEY LTMGHEVTMLPELPIMTWVLS DPSSYKPAPMASWGVPYGQLT EEEKTRAWFTDGSARYTETTR KWTAVAIQPLSRTSLKDSNEGK SSHQQAKNGITVLAGVIDPDYQ DEISL/LTPQWRCHPGSSVWRAS SLGISHPP
3947	34315	A	3988	2	384	CGRSGYWHSSVATKITRLRML RPREGRKLPPGDIMIPLN*KLRL PPGS/FLLLSHQAKKGVTMLAG VTDPDYQDEISLLLHNGGTGKS PHISDTFYGSKVASCQNTGPEK QDETQAQETAVYKSQIFGS
3948	34316	A	3989	3	1273	
3949	34317	A	3990	3	341	GLGRRQPAGSWPERRPGPSA\R RSTAPRRCGQAES*TERGSQPH QVQGQGRWGVCMKIPSHSGKS PDVSEVSKSRNSIISTAVTHAVV APEGLKRNGGGSHLRSSRGHR AVIF
3950	34318	A	3991	44	243	
3951	34319	A	3992	40	558	LGSIQVMQAVRNAGSRFLRSW TWPQTAG*QMTAPSSPPPPPGL CSYSCPLSHP/SLPVTVRPWPSPS FSSQQGRGQNA/APGPSAQALD SSKTLRPSRKLNRTRLPATPSSG EPHLDQPSGDPQPLTLARHPPES EPVNFQLCHLLSVGPYANKSEP QPSHLKMRIMLREVVRIT
3952	34320	A	3993	335	581	RRHLFLQWGQRAWRLQVAAA GTTRPTSAMGIRCSEGAAARAT AARA*TAGPEPLE/PAANPPPPL TASALRAPPSFVLPQCTR

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3953	34321	A	3994	216	1159	SWHGPPGANTVAAAAGPEE\K AALKLRPTHGWPVRATDVHDV ILKASGESEWRGGSRASHQMSP VAMATALGEGVPVRGPAAGSL RLLPGSSAPLGRDAISSCNGVN GLETTGGRCRHNAPNKRHGDP LLEGAAAR/AQAARA*TAGPEP LE/PAANPPPPLTASALRAPPSF VLPQCTAAPRDPSAAGAAN*G KAQSRNC*NEPFAYGGGTHGT GAGAAVTVAADGN*LGSIQVM QAVRNAGSRFLRSWTWPQTAG PWPSPSF/VFPAGSWPERRPGPS AQALDSSKTLRPSRKLNRTRLP ATPSSAFTLPFQERRAL
3954	34322	A	3995	1	738	MTKRGHGTAWAVASKSASPKP WQLPHSVEPVGTEKSRIEVWEP LPRFQRMYGNTWMSGSSLLQG NQNLHAERYCNSTLERNDTPIE SLKPKRESEDGLGEHNGSTMEE VGAETRVQRHWVRVSMTELAL ASDAHMWGSNPGQRVTGVMV GECGTMLGDTQVLLSNPCGDR ARRAYSTAPDYAVCGNGGKVK LNEQRFGSTNKQGKAAYWME ALRPEPLCWQSNYPEAAAVGK PKAAYTKKLHGEDS*AIPVVTE LGERIAQLLIMLYV\KWGKSEIK RT/G/GFGSTNKQGKAAYWME ALRPEPLCWQSNYPEAAAVGK PKAAYTKKLHGEDS
3955	34323	C	3996	87	329	
3956	34324	A	3997	3	122	
3957	34325	A	3998	1	156	
3958	34326	A	3999	1	353	
3959	34327	A	4000	1	201	
3960	34328	A	4001	56	207	EEKKEKEKEKEKEK/EEEEEEEE EEEEEEEEEEEEEEEEEEEEE EEEEEEEEEEEEEEEEEEEEE
3961	34329	A	4002	1	174	MNRC*RHIYSSNEVH*KEEEEE EEEEEEEEEEEEEEEEEEEEE EEEEEEEEEEEIPLSSL
3962	34330	A	4003	1	278	MTSYKFTEPKNGIWQLHEAAQ LDTTYNKLNKKEEEEEE\EEEEE EEEEEE\EEGEGEEEEEEEEEE EEEEEEEEEEEEEEEEEEGVIL
3963	34331	A	4004	144	429	DLPREEYALLPAGPRRRCRHTH RYEPNPEFGAKHSCPAA*HRAA PATSDTQE*HRSNAFGEEEEEEE EEEEEEEEEEEEEEEEEEEEE EEEEEEEEEEEEETLFSNM

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3964	34332	A	4005	3	122	TEEEEEEEEEEEEEEEEEEEE EEEEEEEEEEEEGEEEE\EEEEE
3965	34333	B	4006	1	300	
3966	34334	A	4007	1	1226	MPSSKGVHVHSPPRYLAAKDF KMINKELTAATFMEVIAEDNRF IYDGIDSNFEPELVFLEFFEALLS FAFICVTDQMTKSYTNVPADD VSGNKHETIYTILNQDAQNKSP SAVMSHESDAAHSDSARSSSSK LELSPDVNKIRKSEAMVKEKKK ADKKGEKSARSPSSLSDNLDFS KQDGNTTRQEMSPAGVPLLGM QLNEVKPKKDRQNVQQNEDAT QYEESILTKLIVESYEGEKVRGL YEGEGFAAFQGGCTYRVSCPFE NLQEGEEGRLCEECPDEPRRVH VAGRSMYEGEVVNGMRNGFG MFKCSTQPVSYIGHWCNGKRH GKVGEVATWRAEKKKKEEEEE EEEEEEEE\EEEEEEEEEEEEEE EEEEEEEE\EEEEEEEEEEEEEE EEEEEEEEEEKIRP
3967	34335	A	4008	453	705	LLSIVQAEAVSENSHPILPRVSR SGWGQKEEEEEEE\EEEEEEEEE EEEEEEEEEEEEEE\EEEEEEEEE EEEEEEEEEEEEEEGRRRRRSSP SCYSITPELSCKLGHR
3968	34336	A	4009	93	705	ESSTQTCSGFWTGCTALHRWR GMPERCPPESRDS*TRFPQSSLP GHKT/SEKEEEENRKEEEEEEKE KEK/EEEEEEEEEEEEEEEEEE EEEEKEEEEEEEEQEEEEDDEE EEEEKSCSVNVSLIELPWDPKA YSRLAPLSSQPGPAVKVPTEHLI AKLEDCVQGFTYLTVEKRWAR AVTGAQELGVDYPRNEKCKPH NNGYDND
3969	34337	A	4010	1	3189	
3970	34338	A	4011	1	5127	
3971	34339	A	4012	209	3816	QGRPTFRFRKYREHHKDTPREE QLQDT*SSDSPKLK*RKKC*GQ PERKVKLPTKGSPSD*KRISRQ/ KTLQARRQSWFFEKINKIDRPQ ARLIKKKREKNQIDTIKNDKGD ITTDPTEIQITIREYYKHLYANK LENLEEMDKFLDTYTLPRLNQE EVESVNRPITGSEIEAITNSLPTK KSPGPDGFTAEFYQRYKEELVP FLLKLFQPIEKEGILPNSFYEASII LIPKPGRDTTKKGNFRPISLMNI DAKIL

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3972	34340	B	4013	1	3570	
3973	34341	A	4014	1	2347	MELKTKARELHDECTSLSSRFD QLEERVSVMEDEMNEMNLPTK KSPGPDGFTAEFYQRYKEELVP FLLKLFQSIEKEGILPNSFYEPSII LIAKPGRDTTKKENFRPISLMNI NAKILNKMLANQIQQHIKKLIH HDQVGFIPGMQGWFNIRKSINV IQHINRTKDKNHMIISIDAEKAF DKIQQHFMLKTLNKLVLEVLA RAIRQEKEIKGIQLGKEEVKVSL FADDMIVYLENPTVSAQNLLKL IGNFSKVSGYKINVQKSQAFLY TNNRQTERQIMSELPFTIASKRI KYLGIQLTRDVKDLFKENNKPL LKEVKEDTNEWKNIPCSWVGRI NIVKMAILPKVIYRFNAIPIKLP MTFFTELEKTTLKFIWNQKRAC IAKSIFSQKNKAGGITLPDFKLY YKATVTKTAWYWYQNRDIAQ WNRTEPSEIMLHIYNYLIFDKPE KNKQWGKDSLFNKWCWENWL AICRKVKLDPFLTPYTKMNSR WIKDLNVRPKTIKTLEENLGITI QDIGVGKDFMSKTPKAMATKA KIDKWDLIKLKSFCTAKETTIRV NRQPTTWEKIFATYSSDKGLISR IYNELKQIYKKKTNNPIKKWAK DVNRHFSKEDIYAAKKHMKKC SSSLAIREMQIKTTMRYHLTPV RMAIIKKSGNNRKIQ/GGIWCD RIL*R*TTCRVAKEIQSL*RRI/W KRLQRTLSIPVLDAV*PPMF*AS
3974	34342	A	4015	1	5073	
3975	34343	A	4016	1	3297	
3976	34344	A	4017	1	3514	MELKTKARELREECRSLRSRCD QLEERVSAMEDEMNEMKREG KFREKRIKRNEQSLQEIWDYVK RPNLRLIGVPESDVENGTKLEN TLQDIIQENFPNLARQANIQIQEI QRTPQRYSLRRATPRHIIVRFTK VEMKEKMLRAAREKDRSTRQK VNKDTQELNSALHQADLIDIYR TLHPKSTEYTFFSAPHHTYSKT DHIVGSKALLSKCKRTEIITNYL SDHSAIKLELRIKNLTKSRSTTW KLNNLLLNDYW

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3977	34345	A	4018	1	2666	MVKGSIQQEELTILNIYAPNTG APRFIKQVLSDLQRDLDSHTLI MEDFNTPLSTLDRSTRQKVNK NTQELNSALHQADLIDIYRTLH PKSTEYTFFSAPHHTYSKIDHIV GSKALLSKCKRTEIITNYLSDHS AIKLELRIKNLTQSRSTTWKLN NLLLNDYWVHNEMKAEIKMFF ETNENKDTTYQNLWDAFKAVC RGKFIALNAYKRKQERSKIDTL TSQLKELEKQEQTHSKASRRQE ITKIRAELKEIETQKTLQKINESR SWFFERINKIDRPLARLIKKKRE KNQIDTIKNDKGDITTDPTEIQT TIRESYKHLYANKLENLEEMDT FLDTYTLPRLNQEEVESLNRPIT GSEIVAIINSLPTKKSPGPDGFTA EFY/PESYL*QTHRQYHTEWAK TASIPFENWHKTGMPSLTTPIQH SVGSSGQGNQPGEGNKGYSIRK RGSQIVPVCRRHDCLSRKPHRL SPKSP*ADKQLQQSLRIQNQCT KITSILIHQQQTNREPNHE*TPIH NCFKENKIPRNPTYKGCEGPLQ GELQTTAQGNKRGHKQMEEHS MLMGRKNQYRENGHTAQGNL QIQCHPHQATNDFLHRIGKNYF KVHMEPKKSPHRQVNPKPKEQ SWRHHTT*LQTILQGYSNQNSM VLVPKQRYRSMEQNRALRNNA AYLQLSDL*QT*EKQAMGKGFP I**MVLGKLASHM*KAETGSLP
3978	34346	A	4019	824	3693	AWKGTTDRSTRQKVNKDTQEL NSALHQADLIDIYRTLHPKSTE YTFF/LAPHHTYSKIDHIVGSKA LLSKCKRTEIITNYLSDHSAIKL ELRIKNFTQSRSTTWKLNNLLL NDYWVHNEMNAEIKMFFETNE NKDTTYQNLWDAFKAVCRGK FIALNAHKRKQERSKIDTLTSQL KELEKQEQTHSKASRRQEITKIR AELKEIETQKTLQKINESRSWFF ERITKSDRPLARLIKKKREKNQI DTIKNDKGDIT
3979	34347	B	4020	1	3765	
3980	34348	A	4021	1	4791	
3981	34349	A	4022	1	3297	

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3982	34350	A	4023	1	3170	MVKGSIQQEELTILNIYAPNTG APRFIKQVLSDLQRDLDSHTLI MGDFNTPLSTLDRSTRQKVNK DTQELNSALHQADLIDIYRTLH PKSTEYTFFSAPHHTYSKIDHIL GSKALLSKCKRIEIITNYLSDHS AIKLELRIKNLTQSRSTTWKLN NLLLNDYWVHNEMKTEIKMFF ETNENKDTTYQNLWDAFKAVC RGKFIALNAYKRKEERSKIDTL TSQLKELEKQEQRHSKPSRRQE ITKMRAELKEIETQ
3983	34351	A	4024	281	3030	KPRLENYMKNAEASRADAINW KKGY/LVMEDKMNEMKREGKF REKRIKRNKQSLQEIWDYVKRP NLRLISVPESDRENGTKLENTL QDIIQENFPNLARQANIQIQEIQ RTPQRYSSRRATPRHIIVRFSKV EMKEKMLRAAREKEIQTNIREY YKHRYANKLENLEEMDKFLNI YTLRRLNQEEVESLNRPIRGSEI VAIINSLPTKKSPGPDGFTAEYY QRYKEELVPFLLKLFQSIEKEGI LPNSFYEASII
3984	34352	A	4025	1	3290	MGELITPLSTLDRSTRQKVNKD TQELNSALHQGDLIDIYRTLHP KSTEYTFFSAPHHTYSKIDHILG SKALLSKCKRTEIITNYLSDHSA IKLELRIKNLTQNRSTTWKLNN LLLNDYWIHNEMKAEIKMFFET NENKDTTYQNLWDAFKAVCR GKFIALNAHKRKQERSKIDTLT SQLKELEKQEQTHSKASRRQEI TKIRAELKEIETQKTLQKINESR SWFFERINKIDRPLARLIKKKRE KNQIDTIKNDK
3985	34353	A	4026	1	3573	
3986	34354	B	4027	1	4251	
3987	34355	B	4028	1	3065	
3988	34356	A	4029	965	4089	TWKGTTSTSRCKIMPKYRSTRQ KVNKDTQELNSALHQADLIDIY RTLHTKSTEYTFF/LAPHHTYSK IDHIVGSKALLSKCKRTEIITNY LSDHSAIKLELRIKNLNQSRSTT WKLNNLLLNDYWVHNEMKAE IKMFFETNENKDTTYQNLWDA FKAVCRGKFIALNAHKRKQERS KIDTLTSQLKELEKQEQTHSKA SRRQEITKIRAELKEIETQKTLQ KINESRSWFFERINKIDRPLARLI KKKREENQID

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3989	34357	A	4030	523	3981	
3990	34358	A	4031	1	3429	
3991	34359	A	4032	1	3156	
3992	34360	A	4033	2	4943	
3993	34361	A	4034	1	6747	
3994	34362	A	4035	1	3928	MAAWNLLLKSYAYWGGLRKE DFHCLDRKTLRTVSFLAALLSY ESIGGKGKLTTRKDIYTENPSV HHHHQRPKVDKTTKMGKKQN RKTGNSKMQSASPPPKERSSSP ATEQSWMENDFEELREEGFRRS NYSELREDIQTKGKEVENFEKN LEECITRITNTEKCLKELMELKT KARELREECRSLRSRCDQLEER VSAMEDEMNEMKREGKFRDK RIKRNEQSLQEIWDYVKRPNLR LIGVPESDVENGTKLENT
3995	34363	A	4036	1	3638	
3996	34364	A	4037	3	3585	SNSHITILTLNVNGLNAPIKRHR LANWIKSQDPSVCCIQETHLTC RDTHRIKIKGWREIYQANGKQK KAGVAILVSDKTDFKPTKIKRD KEGHYMMVKGSIQQEELTTLNI YAPNTGAPRFIKQVLRDLQRDL DSHTLIMGDFNTPLSTLDRSTR QKVNKDIQDLNSALHQVDLIDI YRTLHPKSTEYTFFSALHHIYSK IDHIVGSKALLSKYKTTEIITNC LSDHSAIKLELRIKKLTQNRSTT WKLNNLLLN
3997	34365	B	4038	877	8907	
3998	34366	A	4039	1	450	QGSPSGSRE*NSQSSAGPQCALP PAMA*VPLSWRSMGKWWKRT SCTSDST*PPSERRHWRSRKSPS AMPASFRCSSASAREMLP*KKG RCAAGSGIAPGPPETWGRTGGC PGKQATCGVSGPNANGEPVL/K YPSSSSEAHGGPGRNGRSD
3999	34367	A	4040	2	522	
4000	34368	B	4041	102	186	
4001	34369	A	4042	2	5417	

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4002	34370	A	4043	45	1585	KQPSGLLKFGNLILKCHPPSLTH MLSQPCA\EAPTPDPNWELA\LY IHPSSGIMSATVSFWSIGTA\YLE AQGIWEP\FRRRLS\FEASNPPFD VGRPFDLRRIVGISSEGNLNTLS CDPGHSRGFCGAGGSSSRPSAG SHKQ*GPSGHPHSSHSNRNSAD VDDVRAYNSGRTSSMTSAQAA SSQPANKTRPLVLDSNTGAQGH SAGRKSKGAKQSQHGSQHHAH SPLEQHPQPPLPPPVPQPQEPQP ERLSPAPLAHPSHPERASSARHS SEDSDITSLIEAMDKDFDHHDSP ALEVFTEQPPSPLPKSKGSTEGG PASTFTQAVDGGIQFFTDCWTE GPSSSLLAVAREVQLALCIHELL IHGFSQLQVSGGPGAMPDPAAH LPFFYGSISRAEAEEIILKLAGM ADGLFLVRQCLRSLGGYRQLN GTYAIAGGKAHCGPAELCEFYS RDPDGLPCNLRKPCIPPSGLEPQ PGSSTACETPWARPRSRPSSARP RRWRSSLLRRTTSGCPGTTAA
4003	34371	A	4044	1	1773	
4004	34372	A	4045	1	663	MALWTLRPTPLLVTCMLICAPG VMGAVVAPLTILGGPLLIRAAW YTAGIVGGLSTVAMCAPSEKFL NMGAPLGVGLGLVFVSSLVDQ MGRWFVAGGAAVGLGALCYY GLGLSNEIGAIEKAVEYWFNSF VCHSNQQNACSHELHDERLLG DMGLPILHAMLLRRLPSVDSQN ALSSIMLLHTALP*QSAERLFS* TS**EALG*YGFAYPACNASAK TTIRGLTECLIQHHVTPHSIASD QGTHFTAKEVQQWAHAHGIH WPYHVPHHPEAAGL
4005	34373	B	4046	147	330	

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4006	34374	A	4047	485	1568	GEGYKADLAAATVECPICQQQ RLTLSPQYSHIPQGDQPTTW*Q VDCIGPLPSWEGQRFVLTGIDT YFRYGFAYPACNASVKTTIHGL TECLVHHHGVPHGI\ASVQGTH FMA*EVQQWAHAHGIHWSYH VPHHLEAAGLIEQWNGLLMSQ LQHQLGDNTLQGWGKVLQKG VYALNQCSIYGTVSPIARIHGSR NQGVEVAPLKITPSDPLAKCLL PFPKALHSACLEVLVPEGGTLP PGDTTTIPLNWKLRLPPRHFGL LLPLSQKAKKGATVLAGVIDPD YQDEISLLLHIGGKEEYAWNTG DPLGRLLVFPCHVIKVNGKLQQ PNPGKTANDPDPSGMKV*VTPP GKKNPRPAEVLAEGK
4007	34375	B	4048	182	662	
4008	34376	A	4049	1	2250	
4009	34377	A	4050	1	1326	
4010	34378	A	4051	1	1614	
4011	34379	A	4052	1	2586	
4012	34380	B	4053	1	1954	
4013	34381	A	4054	1	705	
4014	34382	A	4055	1	1833	
4015	34383	A	4056	1585	4128	
4016	34384	A	4057	1	1425	MARG/NAITLPV/CGRAVKFT/L EVLRGDSVEKTSRVWSGNERD QELLTEDALDDLIPSFLLTGQQT PAFGRRVSGVIEIADGSRRRKA AALTESDYRVLVGELDDEQMA ALSRLGNDYRPTSAYERGQRY ASRLQNEFAGNISALADAENIS HKAHKYFVFEANTGTETGYQG EESLFNKAYYGGGTNFFRKESQ KLQQSAKKRDAELANGALGIIE LNNDYTLKKVMKPLITSNTVTD EIERANVFKMNGKWDFADFGT TIKQDFRLLGQTSVDRLLQLSQ GQAVKGNQLLPVSLVKRKTTL APNTQTASPRALADSLMQLAR QVSRLESGQQSSKQKKAIQTAI RKNKEANAVLARLNSELQQQL KGFADFREPPIKQDFRLLGQTS VDRLLQLSQGQAITELCGAKRV GYFGPTQFYIALKLIAAAQSGLP VRIESIKCGNSYDHDYEFELGTL VLPRSLEGFALSLNCGEHYWL

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4017	34385	A	4058	1461	2496	NKRNHQSVCHAFIRIP\AAPMV DSLIARVGVMARGNAITLPVCG RDVKFTLEVLRGDSVEKTSRV WSGNERDQELLTEDALDDLIPS FLLTGQQTPAFGRRVSGVIEIAD GSRRRKAAALTESEGTPAFGRR VSGVIEFADGSRRRKAAALTES DYRVLVGELDDEQMAALSRLG NDYRPTSAYERGQRYASRLQN EFAGNISALADAENISRKIITRCI NTAKLPKSVVALFSHPGELSAR SGDALQKAFTDKEELLKQQAS NLHEQKKAGVIFEAEEVITLLTS VLKTSSASRTSLSSRHQFAPGA TVLYKGDKMVLNLDRSRVPTE CIEKIEAILKELEKPAP
4018	34386	A	4059	340	2067	
4019	34387	A	4060	1	1959	
4020	34388	A	4061	1	2319	
4021	34389	A	4062	1	1587	
4022	34390	A	4063	964	1757	GYSGSKPDVITLLEQGKEPCVV ARDVTRRQCPAAPMVDSLIAR VGVMARGNAITLPVCGRDVKF TLEVLRGDSVEKTSRVWSGNE RDQELLTEDALDDLIPSFLLTGQ QTPAFGRRVSGVIEIADGSRRR KAAALTESDYRVLVGELDDEQ MAALSRLGNDYRPTSAYERGQ RYASRLQNEFAGNISALADANN ISRKNITRCINTAKLPKSVVALF SHPG/ELSARAASQRQQCGYHK LHDKQRLLRG*KGNICAKLLNE
4023	34391	A	4064	1	1554	
4024	34392	B	4065	1	1599	
4025	34393	A	4066	1	682	MKRAPVIPKHTLNTQPVEDTSL STPAAPMVDSLIARVGVMARG NAITLPVCGRDVKFTLEVLRGD SVEKTSRVWSGNERDQELLTE DALDDLIPSFLLTGQQTPAFGR RVSGVIEIADGSRRRKAAALTE SDYRVLVGELDDEQMAALSRL GGATQAFAKENNQK\HTKKRT ASLILHAMICCRSLNSSKTKNT KCLNSINQRLKILSLQKDLMCG TAGRCKTLTEQ
4026	34394	A	4067	1	2448	
4027	34395	A	4068	1	2541	
4028	34396	A	4069	1	828	
4029	34397	A	4070	1	1899	
4030	34398	B	4071	1	1686	
4031	34399	A	4072	1	1437	

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4032	34400	A	4073	1	3417	
4033	34401	A	4074	1	3826	
4034	34402	A	4075	812	2578	FIRDFADFGTTIKQDFRLLGQTS VDRLLQLSQGQAVKGNQLLPV SLVKRKTTLAPNTQTASPRALA DSLMQLARQVSRLESGHSNGN GQVSPIFHQTSSSTIRSCSCHLLT LNFLTLQLNTSDIAVFHSTPKLL LVTSTITHMGLNTSQAQSVPVI NSVAGSLAALQPVQFSQQLHSP HQQPLMQQSPGSHMAQQPFMA AVTQLQNSHKFSHRSHGPGQS NDACSEPTNKKMRRNRFKWGP ASQQILYQAYDRQKNPSKEERE ALVEECNRVWQARRLGAFGKE DVHVSFAARRGAKFRHQTLLG RRSSIPAAPMVDSLIARVGVMA RGNAITLPVCGRDVKFTLEVLR GDSVEKTSRVWSGNERDQELL TEDALDDLIPSFLLTGQQTPAFG RRVSGVIEIADGSRRRKAAALT ESDYRVLVGELDDEQMAALSR LGNDYRPTSAYERGQRYASRL QNEFAGNISALADAENISRKIIT RCINTAKLPKSVVALFSHPGELS ARSGDALQKAFTDKEELLKQQ ACKL\HEQKKAGVGDNSIDSW KNAGRVFKDSDKFDANDPILK DQTQEWSGSATFTSDGKIRFIL

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4035	34403	A	4076	1474	3367	REEGANSECLGRHGFKKMLYV KRDEVGKGQIRLETVFEQAIDQ RFSTDTSLSTPAAPMVDSLIARV GVMARGNAITLPVCGRDVKFT LEVLRGDSVEKTSRVWSGNER DQELLTEDALDDLIPSF\LLTGH KTPAFGQRVSGVIEIADGSRRR KAAALTESDYRVLVGELDDEQ MAALSRLGNDYRPTSAYERGQ RYASRLQNEFAGNISALADAEN ISRKIITRCINTAKLPKSVVALFS HPGE\LSARSGKCMVPTESAPH VTVLGCQCGPLGLENGLKEGY LGRSTLDMEAWQPLQEFYLHN LITGQMFEIAVTQNNSKINSSSP TTEQSWMENDFDELTEVGFRR SVITNFSELKEHVLTHRKEAKN LEKSDGENGTKLENTFQDIIQE NFPNLARQVNIQIQEIQKTPQRY SSRRATPGHIIVRFTKVEMKEK VLRAAREKASLAPENLDNSKIR PVVILFHYGESWNLLRADQRLI FAKSWPRASRYQQGHQDLFILR SDLPSQVFIRDKLMERRNRRTG RTEKARIWEVTDRTVRTWIGEA VAAAAADGVTFSVPVTPHTFR HSYAMHMLYAGIPLKVLQSLM GHKSISSTEVYTKVFALDVAAR HRVQFAMPESDAVAMLKQLS
4036	34404	A	4077	794	4235	RVSRGRKWFFIALKRMPAMKK AMNLFLGLSNVRTVHPEGFTV YISTHISFPSLSGYRTGLRSFGLV KQKKSPIRMPCVYTNTLCQYR KPDGSGIVSLKIDWIIERYQLPQ SYQRMPDFRRRFLQVCVNEINS RTPMRLSYIEKKKGRQTTHIDL ALKGLRVLLVEGNDPQGTASM YHGWVPDLHIHAEDTLLPFYLG EKDDVTYAIKPTCWPGLDIIPSC LALHRIETELMGKFDEGKLPTD PHLMLRLAIETVA
4037	34405	A	4078	1	2574	
4038	34406	A	4079	1	536	

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4039	34407	A	4080	368	1449	LKSTNLITFLRLFVPQMPLAYM KFTPSGLVAACAPWLRQRRVV QLGQIAFSAP/YLSQMVRQEMY NRYGESAYEDGYRIYTTITRKV QQAAQQAVRNNVLDYDMRHG YRGPANVLWKVGESAWDNNK ITDTLKALPTYGPLLPAAVTSA NPQQATAMLADGSTVALSMEG VRWARPYRSDTQQGPTPRKVT DVLQTGQQIWVRQVGDAWWL AQVPEVNSALVSINPQNGAVM ALALLNNARPWYLGAQPRDSTI IFCQFGAHPLLDPKTQPVGCRN AARKSCAEIRLVPDARANSGKL VRRYRKYRRQYHKSKSRHQPL RQQQPVRLDWRNVDNQYALT TRFLYQSLQRHAQLNVPLFHVL
4040	34408	A	4081	1420	1842	
4041	34409	A	4082	407	1347	GRIRVHIHKDGRADGGSQPGVT AIQQQLPFAFAFPN*SY*TESAW AQSIK\GPWWLRDQVDGPAGR LAALPQR/SLINAVSTRMEGISG AFNTANPACST*FLCSLLILPSLF STALPNFRLSAMVSDCTISNMV WST/SAVTDWSCTPLD*ERKHR GTARLTTGKGVGMDRDKQVST LFLGFCYAHLQWNEDVFIARH VHLHIALFLDQRAQTASYLQYH IFFARFVFPHRTGVFATVARLK HNDNRTIAPCFTRLWTTLRWR HLLFEVAFVVILQQRQQRVLHI LCIGRIEVHHQTLFKPGDRRKG KQLRFYVLL
4042	34410	A	4083	1	649	MRHGYPARANVLVKVGESAW DNNKDYRYAKALPTYGPLLPA AVTS/ANPQQATAMLADGSTV A/LSMEGVRWARPYRSDT/QQG PTPRKVTDVLQTGQ/QIWVRQV GDAWWLAQV/PEVNSALVSINP QNGAV/MALVGGFDFNQSKFN RATQALRQAGAHLPAHSQSGH HQQTAR*KSNFCARM*TPDQLS W**KNCPFRLSPT*QRQWSLRR YRPVSQRTSF

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4043	34411	A	4084	2	551	WRAAGPEPCPTGRQLRP/AGDL ACSAAAGPGAEPFTAPLALAGR SKCGAAEPAPTQNSRWPMSPH LSLHASPQAEGAGSGL/VPAPR AAAG*RAPQMRP/VVGAEAEE APGP*EPCRHPAPHASQHRYGC HPS/AAEPCRHPAPHASQHRYG CHPSGLNPAGTQHPMPASTGTA AIHRG*TLPAPSSP
4044	34412	B	4085	1	1029	
4045	34413	A	4086	1	2157	
4046	34414	A	4087	1258	1838	TQVVFITSAWGLGEMVVQGAV NPDEFYVHKPTLAANRPAIVRR TMGSKKIRMVYAPTQEHGKQV KIEDVPQEQRDIFSLTNE\EVQE LAQQAVQIEKH\YGSPMD/IEW/ AKDG/HTGNGHVQALRNRCPE ARQHRMRIPGRILPRPIGRMAG PKTRIEHTSVTVISNRRKIKTEN RGHKGYEDRKLHEDLQLRHQS
4047	34415	A	4088	2806	3540	
4048	34416	B	4089	1	1251	
4049	34417	A	4090	341	946	GLSSVGQSVNDHLPWT*GLSSV GQSVNDHLPWT*GLSSVGQSV NDHLPWT*GLSSVGQSINDHLP WA*VLSSVRQSIDDHLPWT*VL SSVRQSIDDHLPWT*GLSSVGQ SVDDHLPWT*GLSSVGQSIDDH LPWT*VLSSVRQSIDDHLPWT* GLSSVGQSVDDHLP*M*GLSSV RQ*VT*AKVNPKISAVTRNRGS VESPHLEGRSLKVQVFIPQVED MSWGPPWLWVEGESWT
4050	34418	A	4091	426	706	VLGGGSEEKAPLWWSGPMVLP GAHSMKT*LPHTHVEFGFACLA SAGAQDVGMEGPRHTTENSVT GSPSHFPPRASQHRRGICRPHAG RATADF
4051	34419	A	4092	596	905	GLSSVGQSIDDHLPWT*VLSSV RQSIDDHLPWT*GLSSVGQSVD DHLPWT*GLSSVGQSVDDHLP WT*GLSSVGQSVDDHLPWS*G LSSVGQSVDDHLPWT*GLSSVG QSIDDHLPWA*VLSSVRQSIDD HLPWT*VLSSVRQSIDD/HSSMD VRSV*CRTISR*PSSMDVRAV*C RTINR*PSSMDVSAV*CKTINR* PSSMDVRSV*CRTISR*PS\P*T* GLSMSLIPSQLCGLSAVTPFSAV TRNRGS\ENHPILKAAASRSKSS FPRLKT

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4052	34420	A	4093	3	1194	SLGPRSHSCCRSDYRSGTTVPL VLLPVCGVPALLVFALLSPLCV VCSALCGGLLPVLRASLFLWCV AFLAGLVFVFGFAFFGSLVRGR FLVVVPFFLLFALCRLLFLVCW LRSFGACPVSVCVAGFACFAGL FLVLVSLLSSGFGFRLSFSCVVG SLCLPGFAFRAFCLFFLPCVGPA LLAFPGFCGPSSPSLSYGGLFAP WSCALLGFFGCLGWSAPGFLSS FGLSVRVLSLPCASGLRSLSGC ALVPGLFLPWVFSPRSLRPLVSF GCLLCSFVSH\NMDWIKES\AG KVIQGNP*WLPVILFFGSVPLTS KAATAKPLMRMG\RALTVSQL T/AVASFAAVYGLFILPT*PTLV GAVQMDDTGTTRIGKLVSNHP FFIRVLLGVALTVCFGFVLGSF
4053	34421	C	4094	70	1950	
4054	34422	B	4095	262	4347	
4055	34423	A	4096	2	458	
4056	34424	A	4097	2	445	QPTERGLCASLKPSRAAIKSQSS KVISFDSMSHIQGTVVQGVGSQ GLEQQYRSGVAVFRLHSFSHRL LSACEFSRCRVQAVSRSIILGSG RWQPPSHSSTREWPSGHTVWG LQPHISPLHCPSKDSL*GLCLCN KLPPENLGFSYVL

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4057	34425	A	4098	1	2589	MVWFLKNVNHGTHTNAKKYN DVENKERTGWKWGSTEYLLCA RPLRKGNVGLSGDVFLTVFVM KTGHSSSLLPSTTTSDSTAQEGY ESRGGMLDWKHLLDSPDSTDP LGAVSSHNHQDKKAMLKDGEE RPFNEPGVFHLLADHQLTQKV ASIPGSAVCAYDMLDIASVFTG RFKEQKSPDSTWTPVPDERVPK PRPGCCAGSSSLERYATSNEFPD DTLNFIKTHPLMDEAVPSIFNRP WFLRTMVRYRLTKIAVDTAAG PYQNHTVVFLGSEKGIILKFLAR IGNSGFLNDSLFLEEMSVYNSE KKWSTAKPVRVTIILNPGQASF CITLRETV/C*RRKHIWCPPYRC TLQ*HFCPCH\CLSGKETLCRVT GGMKVKADRDESLPYAAMLA AQDMAQRCKELGITALHIKHR ATGGNRTKTPGPGA\SRPSSPCP LGCLK/WQTLFPRRRLRWPQGG RRKRSQLEAQRVIRESYLKGHD QLVPVTLLAIAVILAFVMGAVF SGITVYCVCDHRRKDVAVVQR KEKELTHSRRGSMSSVTKLSGL FGDTQSKDPKPEAILTPLMHNG KLATPGNTAKMLIKADQHHLD LTALPTPESTPTLQQKRKPSRGS REWERNQNLINACTKDMPPMG SPVIPTDLPLRASPSHIPSVVVLP ITQQGYQHEYVDQPKMSEVAQ MALEDQAATLEYKTIKEHLSSK
4058	34426	B	4099	1	1299	
4059	34427	A	4100	95	502	FPEIPQSCREGAPGPAKPGGPRA REPCPNRTAASWGVHCEDGGS TVRTGGPL*GRGVHREDGASSP QHPPRRGRGLGHLGPRPL*GQG DAAAAPGHRGKS/GGKGFLPAL RVQRGERGRVSRRAVCMWTSL CASVPS
4060	34428	A	4101	2	653	DSFGSMSVLIKNPRTLFGGKPY VCRECGRGFTWKSNLITHQRTH SGEKPYVCKDCGRGFTWKSNL FTHQRTHSGLKLYVCKECGQSF SLKSNLITHQRAHTGEKPYVCR ECGRGFRQHSHLVRHKRTHSG EKPYICRECEQGFSQKSHLIRHL RTHTGEKPYVCTECGRHFSWK SNLKTHQRTHSGVKPYVCLEC GQCFSLKSNLNKHQ\RSHTGEK

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4061	34429	A	4102	8	389	LPASASQSVGTTGVISFENTCNI CHFFFLLLLFFSSSSSFFFLPFSFS FRVSLF*IQPLKTTASTVQGRQH SGGYRASPERRADQRAHTGEK P/YVCRECGRGFRQHSHLQLSV YPHSFWTQDKRSNH
4062	34430	A	4103	1	740	EGKRGRPFRIPRPAHPFPHELQS RLCILKPLHHPTPSSCPSS*TPVA PLPSHPCAPH/SARSCPVSDEAA L\P*SMALWARAGLLEAPTTLL PAAPDASSPA/MPPSRKLPPPLP L/CPEPLGPSPAAPSPPAPPGPNA AARPPL/PPSPSAAPGPRRPGA\R PVGPSRGPG/PRNSRSLRAPDVH TAPMRCLPSVRPPLPVLSAL/PD PLPRPPSFVPSLPSP/PSSGPSCPP TSAPPGSPRPGFVRLPCLLFWGS
4063	34431	B	4104	48	272	
4064	34432	A	4105	2	622	CPLSPLLFNIVLELLARAIRKEK */LKGIQIGEEEVKLSLFGDDLIV YLENPKYSSKKLLELVNEFNKV SGYKIYVHKSVALLYTNSDQAE NQIKNSTPFTTATSSSSSSSSSP QGIFLTKRLKNF*RGKFKTLVK KNQGDPKKGKNPPGPKMGKN NFGKTPFWAKKI*KFHSI\PKKT PPFFFQKLKKTGVKFFWAPKGP KGFLSKK
4065	34433	A	4106	39	1043	QKQPVWQRCREIGTLGYCGWK WTLDIHGRGHRILSGGVEIPGP WTEGFIQGRDVGELQEPGLSGR ESIH*\GKSYEYECSEDGEVFRV RASLTNHQVIHTAEKPYKCTEC GKVFSRNSHLVEHWRIHTGQK PYKCSECDKVFNRNSNLARHQ RIHTGEKPHKCNECGKAFRECS GLTTHLVIHTGEKPYKCNECGK NFRHKFSLTNHQRSHTAEKPYK CNECGKVFSLLSYLARHQIIHST EKPYKCNECGRAFHKRPGLMA HLLIHTGEKPYKCNECDKVFGR KF\NLTNHQRIHTGERPYKCNA CGKVFNQNPHLSRHRKIHAGE NSLRTLQME

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4066	34434	A	4107	3	941	QQHQQQQHFVGQVAIQQQQQ QGPGVQTNQALGPKPQGLMPP SSHQDLLVQQVSPRPPQGPQG MVGPAQVGVLQHQLHGALGP QGLH*QVFMP\QSRVFSSPQLA QQGQGLMGHRLVTAQQQQQQ QQHQQQGSMAGLSHLQQSLMS HSGQPKLSAQPMCSLLQLLQQ QQLLS*QQHLQQQQQQQLQQQ QQL*QPQLHQQQQQQQLQQQQ PQQL\QQQHQQLQQPQINSQ/HL FPSRRPPNHMGLLTHSPNLTAS LRLTSTHKAALGPGLQAALGHP KDGLLWKTLGTWRARGLICTG GIISYFTQHSWEVKVFTTL
4067	34435	A	4108	1	2255	MEKNKVVKREAEANSINLSVY EPFKVRKAEDKLKENSDNVLE NRVLDGKLSSEKNDTCLPGTAP SKTKSSSKLSSCSSAIMALSAKK AASDSCKEPVANSRESSPLPKE VNDSQARAPLQSTVMTNAVSP AELTPKQVTIKPVATAFLPVSA VNEMKTAGSRVINLKLANNTT VKATVISAASVQSASSAIIKAAN AIQQQTVVVPAPSRANAKLVPK TVHLANINLLPQGAQATSELRQ VLTKAQQQIKQAIINAAASQPP KKVSRVQVVSSLQSSVVEAFN KVLSSVNPVPVYIPNLSPPTNAG ITLPTRGYKCLECGDSFAVEKS LTQHYDRQSMRIEVTCNHGTK NLIFYNKCSLLSHARGHKEKGV AADTRGQKTCTICQMLLPNQCS YASHQRIHQHKSLYTCPECGAI CRSVHFQTHVTKNCLHYMRRV GFRCVHCNVVYSDVAALQSHI QGSHCEVFYKCPICPMACKSAP STHSHTYTQHPGIKIGEPEIIYKC SMCDTVFTLQTLLYRHFDQHIE NQKLSVFKCPDCYLLYAQKQL MMDHIKSMHGTLKSIEGPPNLG INLPLSIKPATQNSANQNKEDT KSMNGKEKLEKKSPSPVKKSV ETKKVASPGWTCWECDRLFIQ RDVYISHVRKEQGKQMKKHPC RHLCQHNRIKHKGIRKVYACSH CPDSRRTFTKRLMLEKHVQLM
4068	34436	B	4109	1	411	
4069	34437	C	4110	54	146	
4070	34438	A	4111	1	1937	

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4071	34439	A	4112	1	1830	MCIEVTCNHCTKNLIVYNKCNL LSQARGHKEKGVVMQCSYSIL KPVSAGHIIVSPSSNSSSSSTLQ SPVGTGIHTVTKIQSGITGTVISA PSSTPSTTAMPLDEDPSKLCRH NLKCLKCNEIFQDKRSLATHFQ QAADMSGQKTCTICQMLLPNQ/ CQRIHQHKSPYTCPECRAICRK KRT\QIHEWERETGKEISISFEKK SMETKKVASPGWTCWECDHLF MQRDVYISHLRKEHGKQMKK HPCRQCDKPFSSSHRLCWHNRI KHKGIRKVYACSHCPDSTGTFT KGLMLEKHV\H*CMASRTLT*K K*QTPPMRRKQK*K*TSRSAVP SG\VERTGSGVQASQRSNNSTT EKAENQCF*GSQAPLCCTQVKG TSASAQAKWGWRR*PTGEQTQ PRGRISQW\VMSDRKCKVCAKT FETKAALNTHMQTHGHAEGCL KQPCRSLLSQPRIKTEARNLIRN ADFLNSILRNGEGYSKEKKNGT GFLGRSARLALGAQGGKSWRF LFWVLLPNVLVLRVGMHDVN HRLINAAGCVSQLAVTLSTEPH GISSAISRVPRHCHPSGENSMAT SLNVNRSISRLAAGSGVLAMDL PIPAGHRAIETGLLGTEDTEQ
4072	34440	C	4113	217	510	
4073	34441	A	4114	210	281	
4074	34442	A	4115	1	675	
4075	34443	C	4116	126	434	
4076	34444	A	4117	804	2061	WERREAGGEDEGINIHEP*VEE EMKKHESNNVGLLENLTNGVT AGNGDNGLIPQRKSRTPENQQF PDNESEEYHSLGDKSKTSFQNS NNNNNKQQEQQQQNPTFSNTR KLTKLYKAPIPPSIILSGCPNIND SNWQEIEHGMQTAGLPTRPLSH GLQQKGAAFRCLGCKCSEPFTG SLILQKAKTNTQKWQATYPKS QNEQLVPSVGKSYRCSTPAQP MKTAVGHKPCKATGAELPKAL GAQPLHPCALDVGQGFKKGNF GAVGLNGLLGLEFHGVSGVLL VGPGDGGLISEGVVREDLMCG VWSAGTWSVGTAERCLEKPGA LHVIEGPLDSWDGPVMPNGPV KSRQSSCLDGPGRCCSEILTGQS HGNKKPARASSKSSQSINDRPL AVLTNQYQCEQLASERQPSSNS

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4077	34445	A	4118	1	357	GKLMLPGSTRKPQVPVDRKMG HEGVFVWQAGLRARPGPSLPFS HGLTLHLHWPLALPV/GATSSP CEAGDLGV\PLAAGTWCPWEA *RQEEAGWQAPGRAGPARVG WGGTGLTSAEVIITI
4078	34446	A	4119	1	771	MLISHKQLSPQLLSLTLPLSEGK AGWAGECPNPPSKDSPVQGIG/ GPPP/GYQKCR*DTASMLTMAP CHGPVCPPHPGWRPRSGSRVIL PAPPGHHPWP\GPRARNGLGTF QGCSTGWQVQETCFGPGGWLG DRHLVGPAATGARCLPAARGP/ DGALHPAVPTGKLKGQP\GPGA RHQRTYD*LPRPCGAAGLGSPP A*HPISEETENQWGLHGPPQPA WARPDHGCQ/APTLSPSLKRKP GRVTAGGPMPGCFSTSSVPTT
4079	34447	A	4120	1	402	MLISHKQLSPQLLSLTLPLSEGK AGWAGECPNPPSKDSPVQGIGD LHQLPKMQIRYSIHADDGSVPR AAHKRGLRKRTLKTISLPRQES AFPFHGQGGDPGVVPGSSFLHP LGTTPGQGPRARNGLG\PSRAA PPAGRGVAGGSPSGG\PAATGA RCLPAARGPVGPYTQQSQRAS* KGSLGPGARHQRTYD*LPRPCG AAGLGSPPA*HPISEETENQWG LHGPPQPAWARPDHGRQPLRC HPP*RGSQGGPQKAAVSQQIPR AGQEGTH*DPTEWGPPDGDQG GPRESCRGLQGGRGQCLCDWS PNTSEI*YPHA*NGD*KAG\PPM DTKSQLQVSTPKSPASHGEDVA RLEEPEASGD/RSVP\GLPGASLI PIWRPPFSRISVRTFLPSPWNLL RDCGFLGTSLASSSGRVTA
4080	34448	C	4121	111	218	
4081	34449	A	4122	2	453	WWPVLSVPPECRLPGRLPSG*V RGPAPWWPEPASQDKSQLSSR GFPGKVSLGKGMAFSPLQTAP* KWLGLSPPLSSTENTASRGHTS PSSRNGFDSQPRDSRTGRECQA TQLPAQHSHAEVLHFGGAMSG QLSLVGPQDSKRTARLTDSQ

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4082	34450	A	4123	1146	1775	KGWLEGAPEA*ERYPG\PPCVV CSLSDAPWVGHPAPSLGV*EP NPP*SRGESQGPTSSICRQSSGD LG*KLESPIHTVIPRHTSQARQG HTAPFPPFQVPS*LLV*LKAVSL APAEAP*PASGLHAPWPVAPRV TCAI/PAKGTTVPAGPAELRPVS PPPILLP/PDSRSSAFPSRKGPASP YETCSPPTS*/EVPS*TYKSMGP GIRLPALPASPRVPSEGPGLSEH PEGPPALPPAIPFS\SPSWFKQCS FSIRPGWLLHGAPQGKGWPQA SWVGKTG*PEKRGSPRGPEHSA LNLRVALPGVAV*EGPACVGW GGPPQPPGAICEATAPPSI/VPPL SLPAPFPGTLP/PPTPAASP/PPAL PPLLRRGRPRPCAALALPALSSL FS/PPVFSLLSLQLPADRVRQVH PVLRAPGPPFRPPKQIPPSSSGDL PFPSLPGR/PVL*LEKWLPPAPK ASPPSSVNLILLVVVKLNTFRCG PLVKNLVPPSVVCPCPCSYKYL *ILIYIHTLHMGQPPSPSSAGNQ SLCYPCGGLVAQPTKRTLVPPTI QLQSVPPPV/KPPCHARPVDSQP PPSLPPPTKHGGAVQAAVWPDS FYPVLLSLG
4083	34451	A	4124	146	1701	TFLGYLETAHGPSAQQCPTGLF AFRSLGRGLLLTSLPKQPARSPP REDVPRSTTQEMTRPRHPPRKP AQPGLGARRRGAPV/RGLSKSR ELNSGNTSDSGNSFT\PPHPRTR GPCWRISPPPAGAESQGDAMLL ARMCQMPSLGLMSRTFPHSST GKARGFQSPCLECAEVKKSSLV PSTARSSPMKGCSRSSSYASTRS SSHSSQSPNPRASPRVRTIITCIL *TRKRPRETKSSAKVT\HYYSSK SGKRSPPSRSSRSRRSPSYSRYS PSSPNSPADIPQNSHPQPSASTD RPHIQSPQFLPTHQGLRNIHVLT PAAPALL*CPPANADTPAQAQP PPLRY*QPSQTLTAAPSSSLRSP LRQRADPIP*PSGGAGSQIQ\WK DSQQRERERARRRRRSYSPMR KRRRDSPSHLEARRITSARKRPI PYYRPSPSSSGSLSSTSSWYSSSS SRSASRSYSRSRSRSRSRRRSRT RTSSSSSSRSPSPGSRSRSRSRSR SRSRSRSQSRSYSSADSYSSTRR

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4084	34452	A	4125	1	1068	MLLLELNAPEHVLETINFQTLT AFCNTFHILRPTKAPGFVYAWL ELISHRIFIARMLAHTPQQKGW PMYAQLLIDLFKYLAPFLRNVE LTKPMQILYKGTLRVLLVLLHD FPEFLCDYHYGFCDVIPPNCIQL RNLILSAFPRNMRLPDPFTPNLK VDMLSEINIAPRILTNFTGVMPP QFKKDLDSYLKTRSPVTFLSDL RSN\LQVSNEPGNRYNLQLINA LVLYVGTQAIAHIHNKGSTPSM STITHSAHMDIFQNLAVDLDTE GRYLFLNAIANQ\LRYPNSHTH YFSCTML\YLFGRRANSGRPFQ\ EQITRVLLERLIVNRPHPWGLLI TFIELIKNPAFKFWNHEFVHCAP
4085	34453	A	4126	1	984	MQANLEMAGNGVTSMGMEPL AIPHIYCCSEGTCNFSNTENHCL RAALSMLLNGTPFAFVIDLAAL ASRREYLKLDKWLTDKIREHGP SVHGLFPSRVLSPALGPGAFPG RHNCGSCVAPQSGLPGVHPVEL PWSISKLFRLRSPANFSDVLGSR SKVLLLMCTLKYCGMQLGADA TRVDMLTFLPTLGFIRNNDYTD DTKASELTELSHNLHAYDSVTG VPGDETECSKTVSTWAYTAESL QGYMAAKLLGRNLTVPSRYLF LNAIANQLRYPNSHTHYFSCTM LYLFAEANTEAIQEQIT/RLVRE RI*S*ANAYWHSEKFYQFTCEL
4086	34454	C	4127	1	399	
4087	34455	A	4128	1	868	MANVCNPSTLGGRGGRITRRPE DPGSPVYSVPPASYHPKPWLGA QPATVVTPGVNVTLRCRAPQP AWRFGLFKPGEIAPLLFRDVSS ELAEFFLEEVTPAQGGIYRCCY RRPDWGPGVWSQPSDVLELLV TEELPRPSLVALPGPVVGPGAN VSLRCAGRLRNMSFVLYREGV AAPLQYRHSAQPWADFTLLGA RAPGTYSCYYHTPSAPYVLSQR SEVLVISWE\TLAPPTTPGGT*S AWGWPGWSSSPWARWSLLTG AVRTALLLFPQVPHRATTPWVT SYDWVWLP
4088	34456	A	4129	1	270	
4089	34457	B	4130	39	919	

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4090	34458	A	4131	3	466	GRALCPPRLLAAGRVLGPGRRS PG\PGPGVP/GG*R*GGAEPRPG APRGRVLPPSAGSGQFSAATPA QNGLPALRGPGSRPGIRSKAVR PVPLGRVGVYFRDALRASGQS GRKLCCIGNTLSPTSFSVGKEVP RKHETNQKHEKGILCMEAVKP
4091	34459	A	4132	1	1647	MWRWLYAGARMTVRDKQPLE QMLAGCTHASLVPTQLWRLLV NRSSVSLKAVLLGGAAIPVELT EQARDMGIRCFCGYGLTEFAST VCAKEADGLADVGSPLPGREV KIVNNEVWLRAASMAEGYWR NGQLVSLVNDEGWYATRDRRE MHNGKLTIVGRLDNLFFSGGEG IQPEEVERVIAAHPAVLQVFIVP VADKEFCHRPVAVMEYDHESV DLSEWVKDKLARFQHLVRWLT LPAEPKNGGIKFHVSAKRVGAL TTRMEAAQQHADDKIRQMINS EQRLSEQFENLANRIFEHSNRR VDEQNRQSLNSLLSPLREQLDG FRRQFRTASLMKVAGWDYLM NSLYNANSSALVNRVRYKWIA AFEGGFTGIVATLDTGRPGPVM AFRVDMDALDLSEEQDVSHRP YRDGFASCNAGMMHACGHDG HTAIGLGLAHTLKQFESGLHGV IKLIFQPAEE\VRVARGRWSMQ VS*MMLIILLPCTLALAYLRALL CAAVIILWQPPNLTRTSPVPPLT QAQNQKTVTMPCWRHTSHSCT ACNRPAQRRSFQS
4092	34460	A	4133	864	1128	TGRSTIRRQRREPRRKAATLRF DRNGCRARCTPP\GRKEQRYQQ TADGDKGAEFYRRPEGVEIVA VMEQRDEVIQADKLAGETKRI DAL
4093	34461	A	4134	618	1102	HSNAAPTARSSFVQNTPSSCGY SRRAWRISSIPEETDRTSYRNIQ CGNHPPVPARLPAGQTGDGDIP PRPRWQSPQTAPRKPPDLP/LIR KNKIPMFRSATTQPGLTGTIAK ASSSEVKAIIGARVKMTRSENF GIQSSLKNILIMSATSWSEPPQP TRLGP

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4094	34462	A	4135	2400	3201	VGGGRNRSPGVACWVEDGNG DAVRDGW\ALDADWQASQAM RRKQQPE\YWQHDAATADADR QMNMPV\LH\RALVAGRAQEM NGAQGKTLLKGW\DEASARRG T\KTED\FCEEDTRDDAMIAWM PR*PGVLPRADAWANVLNHGV GWKKAQLK\STWM\PQVQQ*W RGD\KAANSNAAVAHTVVLLN SGGDATQ/TAAFPISSPLSV/EEV CVTMVIA*FWMWDSGSGGVVL CSSSGRSLTSWSATKVRG/SGH KGRWCSRQGVTCQVRHGGHV APH
4095	34463	A	4136	118	1008	
4096	34464	A	4137	3	1140	KHTYMLSILKPVRTSALPPPAP AQTLCTQLSRVSSRLL*DHPSR WGLR/PSTGMSQARACSPGSLG WMQRSSFTPGAGRVRHIPN\SA GSTRRPACGSRSAAAPVRPCRR TR*G/RSSVVERFMTALSLACR ALPGP*AAPGPSITRRFTISAELK DTRL/PREHVVPLVCTHAIAVPD RGAAVRPTRRRDAAAPPSPLVG DVTLQCPSQ*RGSNAPDQVRLP CVG*RPRSSLQRSGLSVFSADGS TSGPEPASGRKDAGWPARVLRF GTLSRGAPEAGADWGPYSPGSP GAAASGAPWLGQPQALQGAG GQLVGSENGERGTGTKPRVSVS VAYGEIALPADTSWSSRAGAA VLLGLSRSTGGEGPGNMGHGG QSQMLTLEVL
4097	34465	A	4138	10	585	PLEMELNLISIEVWGERLGISTG TEKMPTLKHRTWPVECSKASSL EGDLRSL/S*LEVISAFSADPASA DDSPGCWKKKDDCSMVHLHR QEWQQQQCCQ*K*RKQPPGER RNKCGSHPVCGTVLWQP*QTH\ QISSCPTVGCPPSHSSFSILDGAN AGQEKQSTTEPEPALFLLPPSRG AFGPFGLLSDLRRQL
4098	34466	A	4139	1	474	
4099	34467	A	4140	458	612	ASCMASVDISVLTCMWRCTIEQ SSSFLCLLTPLWE*SWCHVTRIC PFISLG

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4100	34468	A	4141	1	829	MGRPDLILSSILGLRWLLLPQSS RAGRRGAIREASDAEQVTFSGG TVPARTSSGREWRSLLGPDMET TSLFCIDTKTTFLFVYRYGDHIP LVPEQSGLEPLLIWADPGLFHV RLFHLLTIDDNFCGLDMNAPLG VSDMVRGIPVFTEDRDRMTSVI AYVYKNHSLAFVGTKSGKLKK /VRSSAAP*VWDQDTPRSLGQQ GAQRQP/ILRQCVYTFFQLN*RC PHSTARRELRTGGFIPTRSHQD GLRSAARCTQGTTQ*ASWSCV HVCASVRAMCSYC
4101	34469	A	4142	5	237	NFGAMTRIR\DLPWEINPLSSCS SLCEKDPPTTSSPQTN*PKEHHT NFQSETGDEFYPWTQNFSTGHG LGKTVFPWCL
4102	34470	A	4143	1125	1190	
4103	34471	A	4144	306	573	RNFGAMTRIR\DLPWEINPLSSC SLLREKDPPTTSGPQTNQPKKH LTNFKSGKRPLLTLFSNLSHCPS TTFFFPFFNLSLLLISIPFIFW
4104	34472	A	4145	1	329	ASHSWQTLQHSGRYSRSSG/SA GSPRDCAARAPTISPGCAMAWL NLDSISPSSQSKASPLSQLTCPET SYTGCP*SAPHSPPPPWCPQERC ACKGHCLHHRDGCCGYGYN
4105	34473	A	4146	2	336	SILTRKCKYGMEIPT/NIPGLGA AGPTGMFFGSAPSPMGGISPAM TPWNQGATPAYGAWSPSVGSG MTPGAAGFSPPKA/PTYSPTSPG YSPTSPTYSLTSPAISPDDSDEE
4106	34474	B	4147	1	1260	
4107	34475	A	4148	150	335	SFQQSAPW*ASGQSCASDPAPP ATARGRFGPHQSQAFHSRHSPIP DPLPPPCSGGWGHSRW
4108	34476	B	4149	1	3267	

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4109	34477	A	4150	1528	2973	GKQIFSLIIPGHINCIRTHSTHPD DEDSGPYKHISPGDTKTVINNW LLIEGHTIGIGDSIADSKTYQDIQ NTIKKAKQDVIEVIEKAHNNEL EPTPGNTLRQTFENQVIAVVGQ QNVEGKRIP*LPPPL*WGAGRR EGVG*CGRFSEHSRSSAAGYRG GRPCC\PSWEDDP/GAPPDPPAS AQIPAPTRSGCVRCSARPSPGPP AECAAGPSHWYNQSGTSSQKP CWKA*AYPGSGTQRSRGSQAR SHP**SEAESGA*SQMESACPRR SAVQRQQ*PDSQTSAAECSLG WAPAHCCVPSR*PLLRPAWPS* *CSECPGKS*NQQWSPQCQ*YD PNPQSTVVAEDQEWVNVYYE MPDFDVARISPWLLRVELDRK HMTDRKLTMEQIAEKINAGFG DDLNCIFNDDNAEKLVLRIRIM NSDENKMQEVMGVLEVSVSHV
4110	34478	A	4151	459	940	HLPGGGVPGREGGSPDQHVAP GAVSGGAGGGSTRGRGSRRRR PGRPRPGPRQPRRGALPGGEHG LRASARCAARAQQRDPG/TPSC SSWACPTPRRPWAPAASSRLRR PPRGPACATPPPCRPPARRTCTG RCPPSCCLCGSPTTWRRPPPTG GALESPKRR
4111	34479	A	4152	264	1386	SSRCQPVCESGHPGYGQSPA/YT TAGRTESGGTGST/GDNHPLWP CI/GGAPCPAQNTPHLRCV*RSH ALALDSAGSSSPESPH*RASIPH TTLGQKRRSWAGTAHS\PMAPC AAASISTST*LSHHHSPAAQSVC PSSHTTPSFCPIQKFHCFR/SPQR NTS*VVLCPGG*LRVG*WPSSG HDRSWYHTREPSVGN*HRSHQ RR*RGTAPAPGPSARLQCPARG SRSSHSAPASSSRRPFPGSTPAG LGFPSARFPVGKPVVPAALMNR PTRGERRFAYWAPGWFFFSPVR RATADCPSP/SWP*ESCSKRSTL VCPSRRKSCLMVVPKSAKSPVL AK/YGPVGHDHGTEHDVVLGE VQGKRPVAPTMGTPKHKAVHP RAPH
4112	34480	B	4153	52	363	

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4113	34481	A	4154	321	802	HLPGGGVPGREGGSPDQHVAP GAVSGGAGGGSTRGRGSRRRR PGRPRPGPRQPRRGALPGGEHG LRASARCAARAQQRDPG/TPSC SSWACPTPRRPWAPAASSRLRR PPRGPACATPPPCRPPARRTCTG RCPPSCCLCGSPTTWRRPPPTG GALESPKRR
4114	34482	A	4155	15	263	CGRFSEHSRSSAAGYRGGRPCC \PSWEDDP/GAPPDPPASAQIPAP TRSGCVRCSARPSPGPPAECAA GPSHWYNQSGTWKCKG
4115	34483	A	4156	3	518	SPSVGSGMTPGAAGFSPSAASD ASGFSPGYSPAWSPKPGVPGVP QVPSKPLKSLHPGGVVRHLSGQ VCFLHSSG*VCPLLISFVGCFPT GGAMSPSYSPTSPA\YEPRSPGG YTPQSPSYSPTSPSYSPTSPSYSP TSPNYSPTSPSYSPTSPSYSPTSG SYSPTSPSYSPT
4116	34484	B	4157	620	6763	
4117	34485	C	4158	430	870	
4118	34486	A	4159	1	3039	MDSETRRTAKVRLLMTVLRDQ DRVSGVQAHPEQFQQAICPLCG VSLTRSGTTFGSPSEIYSPLGESR ASSGLPRRDGRLIGEEPPEKKFS RSPKGD/LSSGGQRIDYRVCVPT KFNL*VLSF*PRGQGAGGQSPG FSVRRLLVLVWSSGTFV*NGK* QKLL*TLCECVHD*GVQGPASG SPVCSSTAKATEFEKDPSGPFSS SSLPLTPYISFSRVTASSASPGLG SALTPQTLKRKGRI*AICL*VVE TPKVFR
4119	34487	A	4160	1	772	MVARAFLWSQVIRRLGRKGGL SQGDRGCNTALAEGRLDPDLT RGHPALCLPRRPAPRPAEVRRE GEAEQPEAGQPPGAAPRRARD NGAAAAAAGGRLLQSVRPAVV CPHPGPQASYGLRYIAKVLKNS IHEKFPDATEDELLKIVGNLLY YRYMNPAIVAPDGFDIID\MTA GGQNNSDQRKNLRSTAKVLQH AASNKLFEGENEHLSSMNNYLS ETYQEFRFKNVTFDIIATEDVGI FDVRSKFLGVEMEKVQLNIQ
4120	34488	A	4161	174	444	YHRHDSWRNTRR*\IKLDGKGE PKGAEESEATSKYTAAKLHEK GVLLDIDDLQTNQNAVNDFSV GPQDEVIVEDITNCYLCEIFKRY EWVT

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4121	34489	A	4162	379	520	GTSHRGASQRRCCPPLSKTGPK TPCGKGAPSAP*QGGLDVQGEP GGK\GDSSGECVGGNVAGLHK GGGTRADSQVPGGMRGGRMS Y/GG/HLTAEGPMGRSGPR/GAV PSLYPPGFSRGSCSRQYSGAHM PILTGHVGWSESSLDPPRAGQD RFLGTARP*GTSHRGASQRRCC PPLSKTGPKTPCGKGAPSAPFIP AGPTFDHKALM
4122	34490	A	4163	455	798	
4123	34491	A	4164	32	2109	WIGGCPGSQPDATAIMGWTLA PHSSRCHRCCHYRCHCRCCLCP AEMTVGRPEGAPGGAEGSRQIF PPESFADTEAGEELSGDGLVLP RASKLDEVLSPQEEIDPTSDSTG SIYHTLLDLAQKGRWLSVWSLS FSLTQRVMKTSLKMRRTWRVS SKTRTGGWCRSSARRL*GVAPQ GAA/DSLNNLPSNIPRPQTQPPS GSRPPSQHRSVSSWASSITVPRP FRMTLREARKKAEWLGSPASF EQERQRAQRQGEEEAECHRQF RAQPVPAHVYLPLYQEIMERSE ARRQAGIQKRKELLLSSLKPFSF LEKEEQLKEAARQRDLAATAE AKISKQKATRRIPKSILEPALGD KLQEAELFRKIRIQMRALDMLQ MASSPIASSSNRANPQPRTATRT QQEKLGFLHTNFRFQPRVNPVV PDYEGLYKAFQRRAAKRRETQ EATRNKPFLLRTANLRHPQRPC DAATTGRRQDSPQPPATPLPRS RSLSGLASLSANTLPVHITDATR KRESAVRSALEKKNKADESIQ WLEIHKKKSQAMSKSVTLRAK AMDPHKSLEEVFKAKLKENRN NDRKRAKEYKKELEEMKQRIQ TRPYLFEQVAKDLAKKEAEQW YLDTLKQAG\RRKTL*ETRVKA PGLFKRKRPKSRIFPGSKKLQNS ASEIQSR/RLEGSLEQPASPRKV LEELSHQSPENLVSLA
4124	34492	A	4165	251	637	

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4125	34493	A	4166	1	1344	PGRTTRSMAEDVFLSAPIPRGC ADGRDADPTEEHMAQTERNDE EQFECQELL*CHVQVGAPEEEE EEEEDAVLVAEAEAVAAGWM LNFLCLSLCRAFREGRSEDFRRT RNSAEAIIHGLCSLTACQLRTIYI CQFLTRIAAGKTLDAQFENDER ITPLESALMIWGSIEKEHDKLHE EIQNLIKIQAIAVCMENGNFKG AEEVFERIFGDPNS\HMPFKSKL LMIISQKDTFHSFF\QHFSYNHM MEKIKSYV\NYVLSEKSSTFLM KAAAKVVESKRTRTITSQDKPS GNDVEMETEANLGYKKKC*LT NSLR*LNPQRVQYPY*GSHKNL FLSKLQHGTQQQDLNKKERRV GTPQSTKKKKESRRATESRIPVS KSQPVTPEKHRARKRQAWLWE EDKNLRSGVRKYGEGNWSKIL LHYKFNNRTSVMLKDRWRTM KKLKLISSDSED
4126	34494	A	4167	1	1345	IPGSTISCLKGQYPSEPFNMAED VSSAAPSPRGCADGRDADPTEE QMAETERNDEEQFERQELLEC QVQVGAPEEEEEEEEDAGLV AEAEAVAAGWMLDFLCLSLCR AFRDGRSEDFRRTRNSAEAIIHG LSSLTACQLRTIYICQFLTRIAA GKTLDAQFENDERITPLESALMI WGSIEKEHDKLHEEIQNLIKIQA IAVCMENGNFKEAEEVFERIFG DPNSHMPFKSKLLMIISQKDTF HSFFQHFS\YNHMMEKIKSYVN YVLSEKSSTFLMKAAAKVVES KRTRTITSQDKPSGNDVEMETE ANLDTRKRSHKNLFLSKLQHG TQQQDLNKKERRVGTLQSTKK KKESRRATESRIPVSKSQPVTPE KHRARKRQAWLWEEDKNLRS GVRKYGEGNWSKILLHYKF\NN R\TSVM\LKARWRTMKKLKLIS SDSEDWIVFVKL
4127	34495	A	4168	3	378	LTSGSRADQGEGQEEGAEGGR ASSSSSSSSPRGPQHHPHLHGDP AEHRPGHPLCSPPDLTVAYQ/M PEVPAEDM/SDPSFCSARQGGQ RGLDSGPGAPWSSSHSPHSRFQ EASHGACAGWRWCRQEEL

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4128	34496	A	4169	1	1044	SGQEVNKEDGQADVQQDHHA DEDGVGDLARQPHLFHLHLRL CRQCGLLPRLLLGPRLGQPSSLS LAGLGPGLGFGDDGLGLQLGG GLACRLGASERGGLQRGGGRG RGRGLGPG/GPRARAGPQRVGA RAAWCAQHSCGSPGKAPPPAP A/TGAGGACRASMAMRSVAGR AGLRRPAPSDGVTDRLPSPLGS PFQAP/EAQQAVLGHPGPGPLG LRGRPGR*RGATLGPRGLT/PRA AAGSRGAAVGGPLRRRPGRGA PAGSPSSPGSPAAAGASDIPDLA GRSPEPAPWPKCEQCWTPGWQ PGRPVPLPQLWPWRGLSISGSM PLGEGLEDGSDPMTPSCCLPGT
4129	34497	A	4170	1	732	SLTQAGTVSLGLDAEGQEVFVP FSAVLPMVAPNDLVFDGWDISS LNLAEAMRRAKVLDWGLQEQ LWPHMEALRPRPSVYIPEFIAA NQSARADNLIPGSRAQQLEQIR RDIRDFRSSAGLDKVIVLWTAN TERFCEVIPGLNDTAENLLRTIE LGLEVSPSTLF\AVASILGGLCLS FNGSPQNTLVPGALELAWQHR VFVGGDDFKSGQTKVKSVLVD FLIGFRLQRP/VSIVSYNHLGNN
4130	34498	A	4171	1	908	MEKAPPQTQHEGLKSKEHLPE QTDEGKTEYRRVPSLRAVVLFR QRSCIENILRACVGLPPQNHML LEHKMERPGPSLKRVGPVAAT YPMLNKKGPLVWEVSPATLFA VASILEGCAFLNGSPQNTLVPG ALELAWQHRVFVGGDDFKSGQ TKVKSVLVDFLIGSGLKTMSIV SYNHLG\NNDGENLSAPLQFRS KEV\SRSNVVDDMVA\SNP\ML YTPGEEPDHCRMGRNLPE*GSS
4131	34499	A	4172	85	529	ECGARPGSSTRPPARLSPRLFCS AIRAALKTRPAPALACTWRTG* RASLPTTRCAGSGLGTCTAEGS EGCSHPGPLTGTG/RQEACPGT APAGSPSCLHPRGRPRPCPPGTL APRMSCPWPRSPPLTRYLPSGE NLQSKLESLNTSEKF
4132	34500	C	4173	215	324	

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4133	34501	A	4174	2	505	YKCEVCDKVFNQN*FLVCHNR CHTGKKPYSCYECGKTFSQTSS FTCYRRLHTGGKPYKCSEHNK TFG*NSALVIHKAIHTGENPCKC NECGKVFNQKAHLARHHRLHT REKPYKCEECEKVFSRKSHLER/ HKLKRGGVALV/C*ECPTVYQN TSCLRSLSCSYPMSLNG
4134	34502	A	4175	1	6192	
4135	34503	A	4176	2	3389	
4136	34504	A	4177	3	875	GEEAALSLCMHSTDDATRLGA RDTEPLWHVPAQ/ARLSAIAGS SGNKHPSR/QDAAGKDSPNRHS K\GSKPSAGSLRLSSREGEDRTA WTGPRGAVEQEVTGPDLC*GR GQQGLLVGWT**EQKRGQGKP QYSSHSSSNTLSSN/ASSSHSDD RWFDPLDPL/EPEQDPLS/KGCM SLAK/APRPAKPHKPPGSMGLC/ GGGREAAGRSHHADRR/REVSP APAVAGQSKGYR/PKLYSSGSS TPTGLAGG/SRDPPRQPSTLWH RTWYL/YHTASAAVHRGLCRE LEQADQIPPSWYGRRPMGNS
4137	34505	B	4178	108	318	
4138	34506	A	4179	103	540	RRGCESHKTLRRGTSWGLDAR GGGPGPGQVSAGRDGAEVWLS TCDRGHALSGSVEELLFLQN/G ARTER*EGPGEWPRPPPPGLASP ALWRFWAEQVGGSFQELESPS CRTARGSSRTWGSILQNSSWLF QDLGLHLAEGCFLETP
4139	34507	A	4180	33	896	KITRHCTAPGKIRIVPKESQEST PQQDGAPGPGRATSCSARWSPR SWKSHELFCKMEPQVLEEPRA VLQDGAPGPGRATSCSARKGR GPEKPVQGLPN/GSVRAHSGGR AAPQPSPRGHGPGRG*TAAPLP HLCPLTPVLLQG*GPD*WPLGW ATMRPLPLRAQPAPPPPHWML LTPSAPPPGTGKPQGGRGQTSG SCVPATDPHCRLSAPSPGKLGPP CDFLEPP*QRTTNWGSSEAGSP KSRCPRGHVPSGGSKGGIFLSL HFPGAPQSLEFPGSQPHGLIGAS
4140	34508	B	4181	1	625	

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4141	34509	A	4182	160	1149	FASERMKVEPWRAGPGRRAWS EGAGQAPQKRARAGAEPQLPA TPALPGGKMVARRTKLA\RGTR RT\YPEPTV\YAAIPIKFSEKQQA SHYLYVRAHGVRQGTKSTWPQ KRTLFVLNVPPYCTEESLSRLLS TCGLVQSVELQEKPDLAESPKE SRSKFFHPKPVPGFQVAYVVFQ KPSGVSAALALKGPLLVSTESH PVKSGIHKWISDYADSVPDPEA LRVEVDTFMEAYDQKIAEEEA KAKEEEGVPDEEGWVKVTRRG RR\LCSPGLRQPACGCWRGRDG SAA\KRAAQLLRLAASREQDGA SSAA\RKKFEEDKQRIELLRAQR KFRPY
4142	34510	A	4183	2	361	GTMVARRTKLA\RGTRRTGIPS PPC*A\AIPIMCSEKQQASHYLY GRAHGIQQGTKSTWPHKRTIFA FNGPPYCSEQESLSCLQSTCGL VQSVKLKEKLELGWESRSKFFH PKPVPVTEEQ
4143	34511	A	4184	917	1128	
4144	34512	A	4185	1	660	MAWQMMQLLLLALVTAAGSA QPRSARARTDLLNVCMNAKYH KTQPSPEDELYGQ/C/SWRKNA/ CSFTSTTQEAHKN/TSHLYGFN WNHCGEMVPACKRHFIQDTCL YE*PPNLGPWI\RRYAWLPGIQE LAEELNFPGVSAGSNPSSSSIQG WVPGILEPEPFFSTKISQVDQSW RKEWVLNVPLCKEDCEQWWE DCRTSYTCKSNGHKGWNWTSG SNKCQVAAA
4145	34513	A	4186	216	781	MDMAWQMMQLLLLALVTAA GSAQPR\SARA\RTDLLNVCMN AKHHKTQPSPEDEAVWPDP/W MCKGSCRKTKSWNI/HRKSKCE VGLA/WEACSVSAGTGRGPGC GRWVGAPQGP/CPRKCSSG*PT W/VQRSQNMEEMAVVNQSWR KERILNVPLCKEDCERWWEDC RTSYTCKSNWHKGWNWTSAPS AVCDPLL

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4146	34514	A	4187	3	625	QCRPWRKNACCSTNTSQEAHK DVSYLYRFNWNHCG\KMAPDC KRHFHPGTPALYE/CAPHNLGA WDPAGWIQSWRKERVLNVPLC KEDCEQWWEDCRTSYTCKSN WHKGWNWTSGFNK\CAVGAA CPTF\HFYFPTPTVLCNEIWTHS YKVSNYSRGSGRCIQMWFDAS PGATPIEEV\ARFY\VAAMSGAG PWAAWPFLLSLALMLLWLLS
4147	34515	A	4188	1	268	EQGRH/GSSTPVGPRGGPR\GAE HAPKHQGCGDRAGPQVGMDQ RRRDPPRAPAAPRPWCGQRAA LSSLGGSHLCDDA*VQPSAGLG KVLKF
4148	34516	A	4189	2	1632	WKRCPGLPRAAATFPSGSGAG GARREAGGRAPTPGPASPRTAR GHARNSPAPARTAGRTGSAGA WQTPCPAPLFPMSAGLPAACH WNPV*LRALKTG/LEGVLGGSA DTQHNRVTDGSLAPN\AACVYT PKINGNRHPNTCTKMFIVSLDA KGKKWKQPTVHQQRKRETCG LHPRKCLQYTPS*WSTTTGILPS RTPRISCVQFVKKKLGQAGLLG HPGACLLCTLP*\PAGVGTFLFP RGC*GVVH*LETHTCG
4149	34517	A	4190	2	87	
4150	34518	A	4191	3	291	
4151	34519	A	4192	112	286	AWLLWLTSLPWGSLYALALLA NKPAL*SLLLLRYTLLPPHHQC EKVPRWNEPQPTLFP
4152	34520	A	4193	1	933	
4153	34521	B	4194	1	999	
4154	34522	A	4195	135	1160	VWALVRSTLELFHTDDEEEGE YDEVTEEVTEQVYLPAKAKVA QEEEVHPYPSAPPHYYFEEKEW PDPPDLSFLEDTGRKVVAPVTE QHLERLLSVLFRQEFSRLDERD DAVEQLRGVCIRAWEKITSGGE QYPSFSAVKQGPKELYADFIAW NLLRQESLKKVISDSAAQDIVL QLLAFGNVNLDCQAALRPIRGK AHLVDYIKACDGIGAKQDSERF AFTIPVVNNLQPAKHFHYFTDG SSNGKASYSGSKGQNQQPIWIL SRHLKPYHEPDAKEEIPGG/CPR TPWLQPCRD*C*GGP*/PVTSNT R*TQPPTWGQIKKLSQMVEENL RKAGQLVTMTVYWN

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4155	34523	A	4196	502	578	LV*EDCIAERAEVLRNESYGIIID WSP*GMFSLNCTSQSACHGHT MFSW
4156	34524	A	4197	2	408	
4157	34525	A	4198	3	853	LLKVIMSAKIFTKKNENSTERL CGDGEKRGPDFRTERSVWLLR LEEAVAMVQRGSRAPESRVVA QVLTLLDGASGDREVVVVGAT NRPDALDPALRRPGRFDREVVI GTPTLKQRKEILQVITSKMPISS HVDLGLLAEMTVGYVGADLTA LCREAAMHALLHSEKNQDNPV IDEIDFLEAFKNIQPS/LVFEASL GLMGIKPVDWEEIGGLEDVKPE VKTAH/WSLRQKSGHC/RSCAR LPTGLLATLGSGSGSGRATEAV SGPAG*KRASIGGSSQRPRRFPT
4158	34526	A	4199	266	370	AERINSITVFSETLKRFLQASGK *FHRDIHNSRN
4159	34527	A	4200	1	1780	MGDVNQSVASDFILVGLFSHSG SRQLLFSLVAVMFVIGLLGNTV LLFLIRVDSRLHTPMYFLLSQLS LFDIGCPMVTIPKMASDFLRGE GATSYGGGAAQIFFLTLMGVA EGVLLVLMSYDRYVAVCQPLQ YPVLMRRQVCLLMMGSSWVV GVLNASIQTSITLHFPYCASRIV DHFFCEVPALLKLSCADTCAYE MALSTSGVLILMLPLSLIATSYG HVLQAVLSMRSEEARHKAVTT CSSHITVVGLFYGAAVFMYMV PCAYHSPQQDNVVSLFYSLVTP TLNPLIYSLRNPEERSHRGVKL NECNQCFKVFSTKSNLTQHKRI HTGEKPYDCSQCGKSFSSRSYL TIHKRIHNGEKPYECNHCGKAF SDPSSLRLHLRIHTGEKPYECNQ CFHVFRTSCNLKSHKRIHTGEN HHECNQCGKAFSTRSSLTGHNS IHTGEKPYECHDCGKTFRKSSY LTQHVRTHTGEKPYECNECGK SFSSSFSLTVHKRIHTGEKPYEC SDCGKAFNNLSAVKKHLRTHT GEKPYECNHCGKSFTSNSYLSV HKRIHNRWI*/YYCRNFWRKAL IDLSSLR*FERAHTGYISYLLQH
4160	34528	C	4201	18	182	
4161	34529	A	4202	1	389	
4162	34530	C	4203	114	548	

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4163	34531	A	4204	122	735	LRAQQQHN*VLTLHKPACTLST TS*K*LHKIRK*LWHLRDRAPFI FTSEMEYFITEGGK/NPQHFQDF VELCCRAYNIIRKHSQLLLNLLE MNSYNGYVGLLHNILQLEREG LATKEELQQNFPPLSVSLPFDQS INQISEHRSLIFNGQYPYGSCWF RQAVCKLIQKYAGEWGWIATA ELRAEIDLNVLKFTIQVLSWKV QASLQ
4164	34532	A	4205	139	4496	KMAYSWQTDPNPNESHEKQYE HQEFLFVNQPHSSSQVSLGFDQI VDEISGKIPHYESEIDENTFFVPT APKWDSTGHSLNEAHQISLNEF TSKSRELSWHQVSKAPAIGFSPS VLPKPQNTNKECSWGSPIGKHH GADDSRFSILAPSFTSLDKINLE KELENENHNYHIGFESSIPPTNS SFSSDFMPKEENKRSGHVNIVE PSLMLLKGSLQPGMWESTWQK NIESIGCSIQLVEVPQSSNTSLAS FCNKVKK
4165	34533	A	4206	1	3150	MEKPRPLEAPSAWPQDDVQCG VTVGMDGAAVRANRTPWPQD LEQTKWIEIKKSAFTWSSQLSL NRGFLTCKDENNNAGLLRVSS YSSREDQLKNIASDSLFMLPGG LCQSPTGTSHCSNQMETQGQGS PGGAVRGDKALGPEKARQGCG MNGSGKYCKFRVLAIQGKPEC LATLMQPDLGDSPGLREMNVV EHLRASFPVEQWYWRGGQRGE AEGARSSKAENNTSLICNFRLD YAPIEKQWDLHFADYFAEDLK
4166	34534	A	4207	1	1203	

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4167	34535	A	4208	1	1470	MLHSRGFLAEVFGILARHNISV DLITTSEVSVALTLDTTGSTSTG DTLLTQSLLMELSALCRVEVEE GLALVALIGNDLSKACGVGKE VFGVLEPFNIRMICYGASSHNL CFLVPGEDAEQDGTGTSGIGAQ KKKMYANNGAIDRKLLFEATF VTIEKCCDTNQKGDDTHALGQ PIRGHDKSLAGSFCYACRSEEG LSQYRAYDSRGQLIAVKDTQG HETRYEYNIAGDLTAVIAPDGS RNGTQYDAWGKAVRTTQGG\L TRSV\EYD\AAGRVIRLTSENGS HTTFRYDVLDRLIQETGFDGRT QRYHHDLTGKLIRSEDEGLVTH WHYDEADRLTHRTVKGETAER WQYDERGWLTDISHISEGHRV AVHYRYDEKGRLTGERQTVHH PQTEALLWQHETRHAYNAQGL ANRCIPDSLPAVEWLTYGSGYL AGMKLGDTPLVEYTRDRLHRE TLRSFGRYELTTAYTPAGQLQS QHLNSLLTYRHANFAL
4168	34536	A	4209	757	907	RRYCRITVRWQSM/WADNRIA VDAHYPYR*CRS\GRVTEKND\ LIPKG\VIRTDDERTHRYHYDSQ HRLVHYTRTQYAEPLVESRYL YDPLGRRVAKRVWRRERDLTG WMSLSRKPQVTWYGWDGDRL TTIQNDRTRIQTIYQPGSFTPLIR VETATAVMDRILKDHQIVVDIP HGEAWLRDDEERPMILIAGGTG FSYARSILLTALARNPNRDITIY WGGREEQHLYDLCELEALSLK HPGLQVVPVVEQPEAGWRGRT GTVLTAVLQDHGTLAEHDIYIA GRFEMAKIARDLFCSERNARED RLFGDAFAFI
4169	34537	B	4210	1	3258	

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4170	34538	A	4211	281	1571	CQCPGAACPTTSCRVIPHWA\Y DEADRLT/HRTVN\GETAERWQ YDER/GWLTDISHISEGHRVA/V HYRYDEKGRLTGERQT/VHHPQ TEALLWQHETRH/AYNAQGLA NRCIPDSL/PAVEWLTYGSGYL AGMK/LGDT/PAANLDIRIPYAT DPA/GNRLPDPELHPDSTLSM/W ADNRIARDAHYLYRY/DRHGRL TEKTDLIPEGV/IRTDDERTHRY HYDSQ/HRLVHYTRTQYAEPLV E/SRYLYDPLGRRVAKRK/DRTR IQTMYQPGSFTPL/IRVETATGE QAKTQR/RQLADTLQQSDGED GGS\VVFP\PVL\VQML\DR\LESE SSADRVRSFISLANQSKCVEHA Y*RWQCHLGVCWWSSHQIPAV PLTGSVTRWHCHLASSSEAGSV AWLPHLSEGHSNRTSSPELLRS RMCAWHTLSAQSVHLVSLYIL EILALMNSINSL
4171	34539	A	4212	311	788	
4172	34540	A	4213	29	395	RIFHSVI\GVAAHKGGVYKTSVS VHL\AQDVAEIT/LLEGNDPQGT VS*YQGPGRTLIPLEAALRNIAH SLSIPPPKIFAAPTLRHYFALFFC GHSLFAPHIELLEAGTVLQLPQ GPWSSPTSF
4173	34541	A	4214	1	1033	MKMPEAIATKEKIDKWDLIKIK SFFSTPKETINRVNRHHTEWEDI SAIHLSDKGPISYIYKNLTRFTR KKQPHYKVGKGNEQTRILESHP HLLKGLASTPFDSEGVRTERRD IIKDGILTQWLLTSYSARKLGLK STGHAGGIHNWRIAGQGLSFEQ MLKEMGTGLVVPGTAENARSC IRAYFYDIHETLCRQEEMALSV VDDHVREKLIWLRQHQEDMTI LLSEVSAACLHCEKTLQQDDCR VVLAKQEITRLLETLQKQQQQF TEVADHIQLDASIPVTFTKDNR VHIG\PKM\EIRVVTLGIGMGAG KNLLSLF*V*NRVEFHGSPFPTI WFLTWETVGFLK
4174	34542	B	4215	414	1022	

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4175	34543	A	4216	896	1626	NATTIRYEHQRVLKAAQYLHQ QGITRCNSSSTLTSAAPGRVDSP PTSMIVAPALIIRFACFTASISEL CVPPSEKESGVTLRIPITHLMRE LTCRLIRDKSATVTGSHTLVVA RHCCYAAPGGCCLLANWLKPG LFGPIGVLSRRGTSVILPIGGFY QWNPMICPNGVVPMQHG*RRG LAQERPLEEWLPVCRDMLNAF FLPDAETEAAMTLIEQQWQAII AEGLGAQYGDAVPLSLLRDEL AQRLDQERISQRFLAGPVNICTL MPMRSIPFKVVCLLGMNDGVY PRQLAPLGFDLMSQKPKRGDRS RRDDDRYLFLEALISAQQKLYI SYIGRSIQDNSERFPSVLVQELI DYIGQSHYLPGDEALNCDESEA RVKAHLTCLHTRMPFDPQNYQ PGERQSYAREWLPAASQAGKA HSEFVQPLPFTLPETVPLKRYN DSVRAPTCAESRAIFTSTRNNTL QLFFNANFRRPWARGLATNVN DRRASVDHQIRMFHRIYQRVM RATIRKGIRRDVEDPHYSSDAG TYLSPNSRQISNGNWQSHIGRSP SLLLCRTWGLLFTGKLVETRFI WPNRGVIPTGNERYIAHRRFLP MEPDDMPQWRCPHATWLAEA KMFDSLAKAGKYLGQAAKLMI GMPDYDNYVEHMRVNHPDQT PMTYEEFFRERQDARYGGKGG
4176	34544	A	4217	838	1575	CFFLSPSPPSSPPSPNRSQTTEEE TKRQE/ERERKREEEEEKKGRR KETKKRRNRQEGKQHRKEEKE GEKQTKQRTETERETKRRRENE QAKAHKGTRKRKEEQKKAKA ARRRTHKRQNPSRGREGTHPK QRQGKEE/VNRQNKEEAKQKR EEAGRTRR/EDRGRKDDKKERR QQQTEKKAKPKAEHGQERTDT TTKKARQREGRPSERRRREREE/ MSKHDPQNRAEKTNEEKEEGR QHER*TQKSSTGI

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4177	34545	A	4218	1	692	MNALHAEALEMTSQFDQELAA KFEADHEMALLMNKDFDRDRE EQRRLAEQARREHEERIKREAA EQARRDAEAKHKAEIEAAARR EAEEKARAELAERQRIEAEQRA EREKKETEERARREKEEAVAAE RRRQEEAEAARLVEEQRKAEE EARRAADKEHRRTVNRR/GLRR SDCSGHPRRIRTESSAGDRWRQ SAGRAHQILRQT*THTSLTTAS KNGAGLSSNSPTRKRS
4178	34546	A	4219	3	1120	
4179	34547	A	4220	1	831	MVKARKIMETPQPAWEMRVRI CTVDWSKLNPYIPDDFSLIKSEK KYDHPELIVDESNLRVVYAPSR YFASEPKADVSLILRNPKAMDS ARNQALLEGYFSFTATEDQLEQ AKSWYNQMMD/SPEKGKAFEH GNMPA\QMLLQVPYFLRE\ERE H*IIITPILHMRKQEQSG*/RNLP KAAQLSMMQDLQTLLMAASY CSELGHVATQFQGMLACTRNP NSWDRNSETSGKAEGFIPMQLG DVADPSVRCSSVSSLWGHSSPK LLRSVCMANRICVKLQRWT
4180	34548	A	4221	1	1503	
4181	34549	A	4222	1	1113	
4182	34550	B	4223	1	760	
4183	34551	B	4224	1	1755	
4184	34552	C	4225	1	4215	
4185	34553	A	4226	1	3240	
4186	34554	A	4227	1989	2144	
4187	34555	A	4228	1	1203	
4188	34556	A	4229	1	4767	
4189	34557	A	4230	31	512	EYRKSPDIRPIVIQHGEEAEITH HFR*QELADKTLIFEITHREMQR FQPVGTGDIREPVFVFFRWRLT NPFNILEHGEPEGIRVDAAVPR AVIGGLEDHIGVAVQKLQHKTF RYFPFIIQMVKDGVVPEGRPAF VHHLSLFLRIKILAHLTHNTQDF
4190	34558	A	4231	369	918	RPGMSNPWRDLFRTGVDPTND RLSALVEI/YRMMRPGEPPTREA AE/SLFENLFFSEDRYDLSA/VG RMKFNRSLLREEIE/GSGILSKD DIIDVMKKL/IDIRNG/KGEVDDI DHLG/NRRIRSVGEMAENQFRV /GLVRCTGTVPPFLHQQKCEYH L/PQRPVASTLSRYF*HFRLRNF SMPRANEIKKGMV

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4191	34559	A	4232	3	1012	SVVLKIVERVDGYFPSPPLFLGA AFGSHVRSRALPDPCVLFRVTI YLCVLASVARTFSPLLPVSRKK HITPLGGFQLHETHLCLQDCRTI ILRPRLGEFGNKFSQLVDTIDLH \NQHGLAHL*KESARGQYSLLL LGMVSLCALILILWRVVYRSVT CPLADQTQALHRLLDGDIVSPF PETAGVRELDTIGRLMDAFRSN VHALNRHREQLAAQVKARTAE LQELVIEHRQARAEAEKASQAK SAFLAAMSHEIRTPLYGILGTA QLLADNPALNAQRDDLRAITDS GESLLTILNDILDYSAIEAGG\K NVSVQSYVARLEPVAASGWHK YPWLN
4192	34560	A	4233	1	502	
4193	34561	A	4234	1	653	
4194	34562	A	4235	2	300	YALATPPLSV/INQWQLALDKG QLPTF/VAGLAPQHPQYAAMHE SYWPYSALR/EILQRTGMLDGG PKITL/PGDDTPTDAVVSPSAVT NSHGR*VPTLGGVWGL
4195	34563	C	4236	40	105	
4196	34564	A	4237	355	526	
4197	34565	A	4238	116	949	RPGTGRCSAVQLPVLLLRGPHS SHTVGTH\MVDLDSGQLCVYP GNSDESMPAATQARERLLADT AKKKAQIAELQSFVSRFSANA* KSRQATSRARQIDKIKLEEVKA SSRQNPFIRFEQDKKLFRNALE VEGLTKGFDNGPLFKTLNLVL\ EVGENLPVLGTNGVGKSTL\LK TLVGDLHPDSGTVKWSENARI GYYAQDHEYEFENDLPVFEWM SQWKQEGDDEQAVRSILGRLLF SQGDIKKPAKVLSGGEKGRML FGKLMMQKPNILIMDEPPTHP
4198	34566	A	4239	1	319	MVKKMARAPMI\L\ALANPEPEI LACRHGRKEVRPDAIIC\TPGRS DYPNQSETNVL\CFPANVHRIPQ AASHLRAHQSRIPISLMSISAKIL TYLLANQIQFLVKQH
4199	34567	B	4240	263	1390	
4200	34568	A	4241	1	323	
4201	34569	A	4242	3	1855	

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4202	34570	A	4243	2	964	LLKHGVSLYIQDKEGLSALDLV MKDRPTHVVFKNTDPTDVYTW GDNTNFTLGHGSQNSKHHPEL VDLFSRSGIYIKQVVLCKFHSVF LSQKGQVYTWGHGPG\GRLGT WEMNRHAWVPRLVGRD*MVII VSPSWPAAKDHTVVLTEDGCV YTFGLNIFHQLGIIPPPSSCNVPR QGLHNRQNRRYPPVPGSAGPTS MEPSKIRPTGLKFSLTTQQQSEI DLGCSSLCWDYRREPLRLAYW FIKKDIAKDTDEETRRHGVSLYI QDKEGLSALDLVMKDRPTHVV FKNTGSLQFQSIPSCRESQILSEK QGDLFREEPMFGS
4203	34571	A	4244	1	725	FRVDPRVRKHFGLFYAMGIVL MMEGVLSAC*HVCPNYSNFQF DTSFMYMIAGLCMLKLYQTRH PDINASAYSAYASFAVVIMVTV LGVVFGKNDVWFWVIFSAIHV LASLALSTQIYYMGRFKIDLGIF RRAAMVFYTDCIQQCSRPLYM DRMVLLVVGNLVNWSFALFGL IYRPRDFASYMLGIFICNLLLYL AFYIIMKLRSS*KVLPVPLFCIV ATAGMWAC\ALYFFFQNLSSW
4204	34572	A	4245	1	833	MKPVWVATLLWMLLLVPRLG AARKGSPEEASFYYGTFPLGFS WGVGSSAYQTEGAWDQDGKG PSIWDVFTHSGKGKVLGNETA DVACDGYYKVQEDIILLRELHV NHYRFSLSWPRLLPTGIRAEQV NKKGIEFYSDLIDALLSSNITPIV TLHHWDLPQLLQVKYGGWQN VSMANYFRDYANLCFEAFGDR VKHWITFSDPRAMAEKGYETG HHAPGLKLRGTGLYKAAHHI/ KAHTL*VCFHAADKGIPETEKK RRLNWTYSSTWLGRFHNHGRG
4205	34573	A	4246	1	672	GTQNAVNG/VIIFLSWGDAVKS FWIYRGGRKREGPLFHA*Q\FLI YTIIIRAVGSIINYVIANYKLKFI TPGVIDFICTSLIAGILTIKLFLLI NQFEKQQIKKGRDITSARIMSRI IKITIIVGLVLLYGEHFGMSLSG LLTFGGIGGLAVGMAGKDILSN FFSGIMLYFDRPFSIGDWIRSPD RNIEGTVAEIGWRITKITTFDNR PLYVPNSLFSSISVENPG

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4206	34574	A	4247	1	347	PLRP\GQPGPGGAGT/RALRAPP LPSSSELCYGPGQPGRWPRCPQ FPSLPPHSS*LLHTGHWPCTLGY CFIPILRAAPPLPCKCASPVL\SC TYPLPAAPSLPVLVHTSIKCFCF HLQ
4207	34575	A	4248	43	446	VLPAVPRPGQ/PPCVPAPVQAPE PPRPSPGWSQATGSPGPAGAAP SWR\GLPAVPGHTAGVLGPGPP GQRQPGPGGAGTQLCGPHLFL RLLNVAYGPGQPAL/RNVPLQT APALTPSPQHLLCPFLSTHLLNA SVFIC
4208	34576	A	4249	1	1521	RIPESRLPTTAFVQAPWARSGSS GLRRWEKHAGQQVGWWARGP GVRGRQAAGGGAAALTCRGG AGSAVRSCAGLPSLASGSAGCR LHPSYSFGFKVGS/PTVPAALSS *STS/RGREHGGVTVVPVMTQN PRS\PDGPARVEDCEAIA*GTG WL\QQGIGTRPPGTGLGRAR\G APAVPQWNPV\KSCQGPGHPNR LPSHGPSSGEAGRGW/RGLQITP QL/PEVTHRRVLPGDHPATEA\G GFGTG*PGLPGRVPGPGVGGTY QAKALTPLGPVGLLAPASCAQC LQQSADGPGATGHL*ELAESQC RRQPTG\PPGQLAVSGWATVPG VPAAPRPFGPAQQPA/SVPTPSY WA/GSPGAAAWPESHRR*ACD WAW**VLPAVPRPGQ/PPCVPA PVQ\PQSHRGPAHDGARLY*GL PQAEQLHPGGGLPAVPGHTAG VLGPGPPGQRQPGPGGAGTQL CGPHLFLCFLNVAYGPGQPGR WPRCPQFPFLPPILSWNIFGVGT QKKKKKNQSFLKKKKKK
4209	34577	A	4250	167	582	RSLGLAVTEMVPWVRTMGQK LKQRLRLDVGREICRQYPLFCF LLLCLSAASLLLNR*RRSAEPGR RL/SL/LKVQTPGPCCLTVRRPRS CGTGDQWGERAPQRSGLGEHG GASRPEAQAGGVGLIASFPEAS SPELPFSHP

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4210	34578	A	4251	402	1465	DLILSHPTAWFTIKYKPKQLGL QELFPQGHSCAVCGKVKCKRH RPSLLLENYQPWLDLKISSKVE\ ESLSKDLELVLENFVYPWYRD VTDDESFVDELRITLRFFASVLI RRIHKVDIPSIYNQETIKSSNESI *KWIVKARQKVKNTEFLQQAA LEEYGPELHVALRSRRDELHYL RKLTELLFPYILPPKATDCRSLT LLIREILSGSVFLPSLDFLADPDT VNHLLIIFIDDSPAEKATEPASTL VPFLQKFAEPRNKKPSVLKLEL KQIREQQDLLFRFMNFLKQEGA VHVL\QFCLTVEEFNDRILRPEL SNG*NAVSS/WKNCRRFIKHTV WMKVLTKLDLIPSLVEEIPR
4211	34579	A	4252	1	1232	FPGRRFRLVVRLRGAEAASERQ VYSVTMKLLLLHPAFQSCLLLT LLGLWRTTPEAHASSPGAPAIS AASFL*DLIHRYGEGDSLTLQQ LKALLNHLDVGVGRGNVSQHV QGHRNPTTCFSSGDLFTAHNF\S EQLRIGSSELHEFCPTILQQLDS RACTSENQENEENEQTEEGRPS AVEVWGFGFLSVSLINLASLLG VLVLPCTEKAFFSRVLTYFIALS IGTLLSNALFQLIPERSYKNKAQ VDSLPTFLAQAGMLLWRVRIR RRVVDPIRESWMLPFTKIPLWG YGLLCVTVISLCSLLGASVVPF MKKTFYKRLLLYFIALAIGTLY SNALFQLIPENRRKWWQPVHN TFGGSTAWHTDKSIEQSIDTLFD EVKKESEKETPSLQIGDLGPQES LKTFNNTNSPHH
4212	34580	A	4253	3	924	VGACTAAARPLPIPQLQPILHHR GEKSQLWAHSGSSWGFLAVAA VPPSHLCPPLQSRGWKRPP/PLA SAGVLPGCCCCACLVSPSLAQP AG\LGPKPAAPLGPGPWVSVAP CSRPGPCPGTRSPA/P*GHPAMG R\GVHEPRVGPAPPEKAIITETG AGLAERRGQGLGGGSSFRSAEP QGCRSLGPQSPGGDPAHTILRPP SQNGDCAEMHACRLHPAILGT HGTGGLAAQSHAPRALLPSCPS SQQPADGWCSLHLCLPGLLLAP RIHGPSTREGGPGHGTPGPTNP ASSGATRGTRRVRPSVPRSPTL

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4213	34581	A	4254	1	318	VADPVGAARAGGQPLAGRVW PRAGGGHSPRVLGAAGPGPHV CTLRLPGTAIRTEPGAPLACAR AWPGSSPAG/PECLPTSC*P*EG QEPSSHVASLPWGPGVGETQ
4214	34582	A	4255	1	718	FFFFFFSFLCHLYWVSPTPGPHG KLANMANWAPWPS*GLSKLVG KHSCPAG*LPGHARAQASGAP G/ISPDSSAREA*ECT/PCGPGPA APSTRGECPPPSSRPHS/SQQDP GRCSFAPAVPQDAGGQGHWCC APATGHSAPRGCPPARAAPTGS ATPAPPPAACAASSLSMVSAPS R*TTGIASSGTSIPETKHQGTPG TAPAGT/GPGGSTGPKA/PGPAP AHPTRLAGTSGHTAPPTCPPAV
4215	34583	A	4256	702	1026	RSGRTQRAAGVSGSALHQVQS WP\HLKISADQRAGLLF*EHPFP PSASSGCLDVSISSYPVGSD*FIN GMARANGRWKTFTGLHSGKPL GFSDAFCQHHNLIILCWKTW
4216	34584	A	4257	170	1049	RGSGCSAELVPSSRWRPGSRAG AAAGTETPG*PRVYVPAGNGE AGGPGAAWARRAAALPGTAA GPPRPAARPGAAPARGGPAPGA PAQALPR/TPTWPAAR*AQRAP SPPSWGS\AQPGHPGDLAAGVG RGAGGGHSRRGRHHHVRSLAD LLQLPGAAEGAGDRGHLPGPD/ GERS*AASSFSAAGRAAGTASC CSAGGTPPSPCTILSTSSSSLAH VASSS/RRRAEGDTKVS/RGRAE GQDSETGREPGVLHRGSGRTQ RAAGVSGS/RSAPSPVVATTSRS LLTSVQGCFSENILSP
4217	34585	A	4258	178	556	QSPQEHFHPECGRRDILCQVRQ EIRWPNPGEVHHLGLEICPVWI LQLHLALRTRAPEHPLQVHRPG GGAV*RGVPPPLRLLQACDGPE VPAAGRPRPARSSPGQWPP*/PA AVAPPVTERPPTPSAA

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4218	34586	A	4259	5	1044	TGRILDGWHWAKELRLDCPLG DSRRPPFSRVSTEGSPAFLALRL PNVTAGS*EVSMLASTETPLVIT RPSPG\GHDPGPAPRGAAASPA GSPAP*QKSPRPLSAAAPPLLAS DPAPPRAAAPPADTESSVQPPA APHAGPWT\PSAPGPLDVHSPPP \PSRGPFVQSSAEPHNRPSPGAT RPRP\PPRGAAASPAGSPAP*QK SPRPLSAAAPPLLASDPAPPRAA APPADTESSVQPPAAPHAGPWT LERSWAP*RSLPTPIPVADPLCR APLSHRYP*GDCQRSGLCHTSP GRASHLPGPGAHKRTPHACWL PLECHRRSPHP*THPSG*PGPSP QSFFPEFLGSGP
4219	34587	A	4260	2	576	CLVNSTTRRSFQLRLVPVPKFQ PPHMTVR*LFNFGRQLTATTFS/ LRKSYAVREAYELQNCPDPPPF QNGYMINSDYSVGQSVSFECYP GYILIGHPVLTCQHGINRNWNY PFPRCDAPCGYNVTSQNGTIYS PGFPDEYPILKDCIWLITVPPGH GVYINFTLLHTEAVNDHIAVW YENLSSQNICDCDQQF
4220	34588	A	4261	1	837	MWAGNAWRAALSGVPCGRSA QSVLAQLRGILEGELEGIRGAG TWKSERVITSRQGPHIHVDGVS GGILNLTSVRFIRGTQSIHKNLE AKIARFHQREDAILYPSCCDAN AGLFEVLLRPEDAVLSDELNCA SIIHGICLCKAHKYHYCHLDVA YLETKLQEAQKHRLFLVATDG AFSMDGDIVPLQKICRLASRYG ALVFVDECHATGFLGLTGQGT DELLGVMGQVTIINSTLGKALG GASGGYTTGPGPLVSLL/RAQP YLFSNSLPPAVVGCTSKAL

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4221	34589	A	4262	1	2142	MIILIDAEKAFDKIQQPFMLKTL NKLGIDGTYLKITRAIYDKPTA NIILNGQKLEAFPLKTGTRQGCP LSPLLFNIVLEVLAQAIRQEKEI KGIQLGKEEVKLSLFADDMILY LENPIVSAQKLLKLISNVSKVSG YKINVQKSQAFLYTNNRQTESQ IMSEFPFTIATKRIKYLGIQLTRD VKDLFKKYKPLLNKIKEDTNK WKNIACSWIGRINIMKMAFPR WELNNENTWTQEGEHHTLGPV VGWGKRGGIALVDIPNVNDKL MVLEVLARAIRQKKEIKGIQLG KEEVKLSLFADDMIVYLENSIV SAQNLKLISNFSKVSGYKINVQ KSQAFLYTNNRQTESQIMSEFP FTIATKRIKYLGIQLTRDVKDLF KENYKPLLKEIREDTNKWKNIP CSRIGRINIMKMAILPKVIYRFN DIPIKLPMTFFTELEKTTLKFIW NQKRACIAKTILSKKNIAGGITL PDFKLYYKATVTKTAWYWYQ NRDIDQWNRTEASEVTSHIYNH LIFYKPDKNKKWGNDSLFNKW CWENWLAICRKLKLDPFLTPYT KIHSRWIKDLNVRPKTIKTLEEN LGNTIQDIGMGKDFMTKTPKA MATKAKVDKWDVIKLKSFCTA KETTIRVSRQPTEWEKIFAIYPS DKGLISRIYKELKQIYRKK\TNN PIKKWAKNMNRHFSKEDIYAA NRQMKKCSSSLVIREMQIKTTM
4222	34590	A	4263	1	1989	
4223	34591	A	4264	1	1104	
4224	34592	A	4265	1	879	
4225	34593	A	4266	1	1659	
4226	34594	B	4267	1	1500	
4227	34595	B	4268	1	1962	
4228	34596	B	4269	1	1716	
4229	34597	A	4270	1	1152	
4230	34598	A	4271	1	4752	
4231	34599	A	4272	1	2790	
4232	34600	A	4273	1	3477	

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4233	34601	A	4274	1	1007	MLDASCHRTSDSKFFSFGVQTG FLTPELAHLVGPCDRDHNSSPA REQNWTENEFDELTEVGFRKW VITNSSELKEHVLTQSKEAKNL EKRAIKQEKEIKGIQLGKEEVK LSLFADDMIVYLENPIVSAQNL LKLISKFSKVSGYKINVQKSQA LLYTNNR\SQIMSELPFTIAMKR IKYLGIQLTRDVKDLFKDNYKP LLKEIREDTNKWKNIPCSWLGR INIMKMAILPKAIYRFNAIPIKLL *TFFTELEKTTLNFIWNQKRARI AKTILSKKNKAGGITLPDFKLY HKATVTKTAWYWYQNRYIDQ WNRTEASEITPHIYNHLIFDKPE
4234	34602	A	4275	737	2460	RIKYLRIQLTRDVKDLFKENYK SLLNEIKEDTNKWKNIPCSWIG RMNIIKMAI/LPKVIYRFNVIPIK LPMTFFSELEKSTLKFIWNQKR ARIAKTILSQKNKAGGIMLPDF KLYYKATVTKTAWYWYQNRD IDQWNRTEPSEMTPHIYNHLIFD KPDKNKQWGKDSLFNKWCWE NWLAIGRQLKLDPFLTPYTKIN SRWIKDLNVRPKTIKTLEENLG NTIQDISMGKDFMSKTPKAMA TKAKMDKWDLIKLKSFCTAKE TTIRVNRQPTEWEKNFAIYSSD KGLISRIYKQLKQIYKKKTNNPI KKWAKDMNRHFSKEDVYAAN RHMKKCSSSLAIREMQIKTIMIY HLTPVTMAIIKKSGNNRCWRG CGEMGTLLYCWWDCKLVQPL WKTLWQFLRDLELGIPFDPAIP LLGIYPKDYKSCCYKDTCTPKL ARDDQIHILKQHRRKELETRQK QYRAWYEINPFHSVWPVTAGK SPRHQLPVWVHNPQTSPYLQL QTRDGEESNENNFGSTILASDFF AEIDKLSILQIHMEMEGTQNSQ NNLDKKKTKMEDLHFSISKLLH SYSIQDNVISA
4235	34603	A	4276	3	355	RQPVHLVHELPQQSWGICLNSS EQHGALQHSSLHL/RMCSEPWS SADPQ*R*TCRNL*LPVRGPPRR TDLFSVSSKSTLKEWPLLLMIL AELGSYLILSGRREESYFTSLVL ISIGDC
4236	34604	B	4277	78	791	

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4237	34605	A	4278	1	3395	MIISIDTENAFEKIQQPFMLKTL NKLGIDGTYLKIIRAIYDKPTAN IILNGQKLEAFPLKTGTRQGCPL SPLLFNIVLEVMARVIRQEKEIK GIQLGKEEVKLSLFVDDMIVYL ENPIVSAQNLLKLISNLSKVSGY KINVQKSQAFSYTNNRQTESQI MNGLPFTTASKRIKYLGIQLTR DVKELFKENYKPLLNEKKVDT NKWKNIPCSWIGRIN\ILKMAIL P/KELEKTTLKFIWNQKRACIAK SILSKKNKAGGITLPDFKLYYK ATVTKTAWYWYQNRDIDQWN RTEPSEII\PHIYNHLIFDKPDKN KKWGMGSLFNKWCWENWLAI CRKLKLDPFLTPYTKINSRWIK DLNVRPKTIKTLEENLGNTIQDI DMGKDFMSKTPKAMATKAKID KWDLTKLRSFCTAKETTIRVNR QPKEWEKIFAIYSSDKGLISRIY KELKRIYK/KKNNPIKKWAKD MNRYF*KEDIYAANRHMKKCS SSLAIREMQIKTTMR/YHLTPVR MAIIKKSGNNRWEMNNENTWT QEGEHHTLG/HC/WWKARRSRS CLTWMAAGKKRMRKTLQMT
4238	34606	B	4279	1	2011	

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4239	34607	A	4280	1	2661	MTMNFVADSHTGRNPLASAAG AKTGLRPLPRPCGARVWNPPD AGGGGVGSLKTSTPLGPLSAAN SPVHQGSVPQTRARGGGTLFQE VVTSRTLAFRNSLSAFTEVTSG TVSGRKGGRSTHLAGRRVSGG EGSRKAAAAALAAVAAAPGPV RRCSSQSCFSSSGSSHYSARTSP VRVRPRRSLSSRSAAGNRAEAT ESAMEKTLETVPLERKKREKEQ FRKLFIGGLSFETTEESLRNYYE QWGKLTDCVVMRDPASKRSRG FGFVTFSSMAEVDAAMAARPH SIDGRVVEPKRAVAREESGKPG AHVTVKKLFVGGIKEDTEEHHL RDYFEEYGKIDTIEIITDRQSGK KRGFGFVTFDDHDPVDKIVLQK YHTINGHNAEVRKALSRQEMQ EVQSSRSGRGDGYGSGRGFGD GYNGYGGGPGGGNFGGSPGYG GGRGGYGGGGPGYGNQGGGY GGGYDNYGGGNYGSGNYNDF GNYNQQPSNYGPMKSGNFGGS RNMGGPYGGGIWKNTSITERK KSRKLDLIQSKKGSRTKEAPQP PVASLCMHLGHWSRLMVSPGA QLTGKNSHGLSVSSVRKSNVGP RRLCAAMKATGPDNAQSQVSP PGHAPSAEDPTGSRTVSSPCTD RPHPFLSRPKPPTQISLVLPLKT DGALERMPQQL/HIASS/GAKVP NPSTQTPPVLLAFFYPFNLPP*N
4240	34608	A	4281	1	908	MRKVKGKNRQSFKCLPPPSGA LQAHGAAAPHGSLLTLHLHLV PVSSAAMKATGPDNAQSQVSP PGHAPSAEDPTGSRTVSSPCED RPHPFLSWPTWISLALLLKTDG ALERMPQQLPSLHPSQGTQSIH PDPSSTSSFLLPFQPPTLKRAAFP CPPSIVNPAVWDTSTPSVAEHH TPIRITLKEPTQFLSQKQYPIPQA ALVGLQPIISHLLASHLLRPTDS PFNTPILPVKKPNGTYRLVQDL RLINQAVLPLVQE/DYSVLLYLP LNVTPGLPPATAFSYPPSPGPVA RARLASRLHSHAA

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4241	34609	A	4282	1	915	MPNYVTFTDTKQLISDTPNNQV PMNRASMAFDAKCLTGCRFDD AIVQFDMTYWPFTVVNDAGRP KVQVEYERDKKLLPIGGVFYGS DKDEGNCKSLPWEDCYQCCET SQNVQDFLFLDVTPLSLDIKTA DGVMAVLIKCDATIPTRQTQTF TTYSDKPSM/LIAKDKNLLRKFE LTGVPPAHHGAHQIEVTFDINA KGILNV\TLTDDKGHLSKEDIEP MVQETEKYKAEDEKQRDKVSS KNSLDPYVFNMKATAEDEKLQ VKINNEHKQKILSKCHEIINWL DKNQTAEKEEFEHAQQELEKSS
4242	34610	A	4283	1	994	MHQTKKGNQWHFGMKAHIGV DAKSGLTHSLVTTRPNEHDLNQ LGNLLHGEEQFVSADAGYQGA PQREELAEVDVDWLIAERPGK VRTLKQHPRKNKTAINIEYMKA SIRARVEHPFRIIKRQFGFVKAR YKGLLKNDNQLAMLFTLANLF RADQMIHCTRGEGLITTKIPKAP DNGSYCLPSKNDDSEEEDPEMS PMVVTKMKEIAEAYLGKTVTN AVLTVPAYFNDSQRQAT/KKDA RTIAGLNGLRISNEPTAAAIAYG LNQKVGTERNVLIFDLGGSITPR IRTPETGSDDAIKSILEQAKKEIE SQKGGECDPCRQSLRPPGPAAN
4243	34611	A	4284	3	677	
4244	34612	A	4285	30	365	EEAETVLVGQLKQLSSCLAVH KYRPETKQEKKQRLLARAEKK AAGKGDVPTKRPPVLRAGVNT VTTLVENKKAQLV\CRKMGVP YCIIKGKARLGRLVHRKTCTTV AFTQVN
4245	34613	A	4286	3	432	NSRVDDFVAAQDAKGKKVAP APAVVKKQEAKKVVNPLFEKR PKNFGIGQ\QRLLARAEKKAAG KGDVPTKRPPVLRAGVNTVTT LVENKKAQLVVIAHDVDPIELV VFLPALCRKMGVPYCIIKGKAR LGRLVHRKTCTTVAFT
4246	34614	C	4287	62	217	

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4247	34615	A	4288	2	801	PKGKKAKGKKVAPAPAVVKK QEAKKVVNPLFEKRPKNFGIGQ DIQPKRDLTRFVKWPRYIRLQR QRAILYKRLKVPPAINQFTQAL DRQTATQLLKLAHKYRPETKQ EKKQRLLARAEKKAAGKGDVP TKRPPVLRAGVNTVTTLVENK KAQLVVIAHDVDPIELVVFLPA L\CRKMGVP\YCIIKGKARLGRL VHRKTCTT\VAFTQVNSEDKG\ ALAKLVEAIRTNYNDRYDEIRR HWGGNDLRPK\SVARIAKLEKA KAKELATKLG
4248	34616	B	4289	1	273	
4249	34617	A	4290	1	441	
4250	34618	B	4291	47	482	
4251	34619	A	4292	1	762	
4252	34620	A	4293	1	890	MSKSESPKEPEQLRKLFIGGLSF ETTDESLRSHFEQWGTLTDCVV MRDPNTKRSRGFGFVTYATVE EVDAAMNARPHKVDGRVVEP KRAVSREDSQRPDYFEQYGKIE VIEIMTDRGSGKKRGFAFVTFD DHDSVDKTVIQKYHTVNGHNC EVRKALSKQEMASASSSQRGRS GSGNFGGGRGGGFGGNDNFGR GGNFSGRGGFGGSHGGGGYGG SGDGYNGFGNDGSNFGGGGSY NDFGNYNNQSSNFGPMKGGNF GGRSSGPYGGGGQYFAKPRNQ/ GGYGGSSSSSSYGSGRRF
4253	34621	A	4294	1	1674	
4254	34622	A	4295	1	506	KYHTVNGHNCEVRKALSKQEI ASASCSQRGRSGSGNFGGDRG GGFGGNDNFGRGGNFSGHGGF GGSCCGGGYGGSGDGYNGFGN DASNFGGGGS/YNEFG/NYNNQ SSHFGPLS/GGNFGGRSS/SPLGG APASTYVKGPNSQRTQNEGWF EG*APWRGDGGARGNKGGGA

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4255	34623	A	4296	1	1445	MKCLKFINHKEILEASERKQAE SLDFPFKKLRWHLCEGWIEEER DESRKSETIFKDLFKVPVLKETI YYKFYGPPVYQIETVYFMALSP PKSKQFDKTKQNNNNKKTHQF VIVFFKTDEHLSARGRRRRSIVK VSLLPAVIGLKSKFLKKPDQLR KLFI\GG\LSFETT\DESLEEPFSR QWGKRYTDSVVMRDPNTKRSR G\FGFVTYAT\VEEVDAA\MNA RPHKVEWKELLEPKRA\VSRED SQRPGCPH*LVKKIFVGGIKEDT \EEHHLRDYFEQYGKIEVIEIMT D\RGSGKKRGFAF\VTFD\DHD\S VDKIVI\QKYHTVNG\HN\CEV* KSPVKSKKMASASSKPKEGRSG FWETFGGGSWEVGFGGN\DNF GRG\GNFSWSVVAFGGSRG\GG GYG\GSGDG\YNGFGNDG\SNF G\GGG\SYNDFG\NYNNQ\SSNF GPMKGG\NFG\GRSSGPYG\GGG QYF\AKPR\NQGGYGGSSSS\SN
4256	34624	A	4297	1	920	DPGDTPNTASAPNCRSGKGRSS SPEHIPPLEKLEDSMQTNPSTNP EPGRLAEWLDPEERQQSLQFGL QEATSIGKGGQYYIKGTPHGTK ESEQQPSALDLPSDRAYPNEKE PENQLWRLVIKLIKEAPEKGAY LNVIKAVYDKPTNGEKLRAFPL RTGTKHRCPLSPLLFNILLEVLA RAIRQEKEIKSIQIGKEEVKLSLF ADDIIIYLESPKYSSRKLQELIKE FSKVSRYEINVHKSVALLYT\NS NQAENQIKNSASFTIAAKNKIK YLGIYLTKDAKDGYKENYKTL MKEIIDDKNKQKYIP
4257	34625	A	4298	1	1194	
4258	34626	A	4299	3	1834	
4259	34627	A	4300	285	502	
4260	34628	B	4301	77	1306	
4261	34629	A	4302	1	354	
4262	34630	A	4303	1	1182	
4263	34631	B	4304	1	1995	
4264	34632	B	4305	1	1518	

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4265	34633	A	4306	1	918	MCPVGPWTHPVVISPVSECIVGI DILGSWQNLHIGSLTDITMVHYI DDMMLIGSSEQEVANSLDLLV RHLHARGCKINPTKIQGTSTSV KFLEFQWCGVCQDIPSKWVLE QKALQQVQAAVQAALPLEPYD PADPMVLEVSVADGVAVWSL WQAPIARIHGSRNQGVEVEVSP LTNIPSDPLAKFLFPAPSTLCSA GLELLVPEGGTLLPGNTTMIPL NWKLRLVPGYFGLLLALSPQA KNGVTVLAEVIDPDYQDEITLL FHNGGGEEYARNTGDPLRHLL VLPSPMIKVNGK\LQHPNPGRT
4266	34634	B	4307	1	1599	
4267	34635	B	4308	1	1569	
4268	34636	A	4309	3	422	
4269	34637	A	4310	1	1089	
4270	34638	A	4311	2	549	LKMTAMQRPMEKRMMNREIIL KERLSLTGIDIKILKKRSIMKVE SHRGEQISVSSLALQRIKYLGIQI TRDVKDLFKENYKPLLNKLKE DTNKWRNVPCPRVGRISIVKM AILPK/ILKKKTTLKFIWNQKRA HIAKTILSKKNKAGGITLPDFKL YYKAT/KTAWCWYQNRDTDQ WNRTKPSEI

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4271	34639	A	4312	371	3036	LIAYQPKKVQDQMDSQPNSTR VLEVLARAIRQEKEIKGIQLGK/ EEVKLSMFADDITAYLENPIVS APNLLKLISNFSK/VSGYKINVQ KSQAFLYTNKRQTE\QIMSELPF TVASKRIKYLGIKLRRDVKDLF KENYKPLLNEIKEDTNKWKNIP CSWIGRINIVKMTILPKVIYRFN AIPIKLPMTFFAELEKTTLKFIW NQKRAHIAKTILSQKNKAGGIM LPDFKLYYKATVTKTAWYWY QNRDIDQWNRIEPSEIIPHICKH LIFDKPDKNKKWGKDSLFNKW CWENWLAICRKLHLDPFLTPYT KINSRWIKDLNVRHKTIKTLEE NLGNTIQDIGMGKDFMTKTPK AMATKAKIDKWDLIKLKSFCT AKETTIRVNRQPTEWEKIFATY SSDKGLISRIYNELKQIYKKKTN NPIKKWAKDMNRHFSKEDIYA AKKHMKKCSSSLAIRETLYNDR RIGKLTQTCDETAFQPHVCTISR PMLSSPYRSSLTEKWSQDFSKP PYPFLFHKGYLNPREQDKEVLT RAIRQEKERKGIQLGKEEVKLS LFADDMIVYLENPIVSAQNPLK VVSNFSKVSGYKISVQKSQAFL YTNNRQTESQIMSELPFTIASKR IKYLRIQLTRDVKDLFKENCKP LLNEIEEDTNKWKNIPCSWIGRI NIVKMAILPKVIYRFNAIPIKLP MTFFTVLEKTTLKFIWNQKRAH
4272	34640	B	4313	1	1995	
4273	34641	A	4314	3	549	
4274	34642	A	4315	3	614	EAYGQTECTGGCTFTLPGDWT S\GQFINILEMCLELSPCKSFSAD SARYVLGHVGVPLACNYVKLE DVADMNYFTVNNEGEVCIKGT NVFKGYLKDPEKTQEAL\DSDG WLHTGDIGRWLPDIENHNRLIV CTLTNTSWRSHKIIVLKTYQKA DDTKTPKETTFQNIMNLFLKEK RATAVLIRGGVGETSTDLSKKK PAKLLANF
4275	34643	A	4316	1	478	MKLDLHLSPYTKINSRWIKDLN LRPETIKILEDIIRKTLLDIGLGK DFMIKNPKVNATKTKINKWDLI KLK\NFCTAKEISSREIREPTEW EKIFANSASDKGLISRIYKELKQ IRSTLQLLFGISELPASLFLGFGA IMKSKKASLNTSTAILRQLIW

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4276	34644	A	4317	1	1125	MCHGIGAQIIPSHQTVQLDITAF LKTVKKNKHKFYPAFIHILARL MNAHPEFRMAMKDGFIENMFF VSANPWVSFTSFDLNVANMDN FFAPVFTMGKYYTQGDKVLMP LAIGGPLESPDRDGGPLESTNR DASPESWSCRKSTPRLVAWVS AAKVFIRDKLMERRNRRTGRT EKARIWEVTDRTVRTWIGEAV AAAAADGGGFRVDLARRSIRK DRNARSQNPVHTEGDMNMNIK KIVKQATVLTFTTAFLAGGATQ AFAKENNQKAYKETYGVSHIT RHDMLQIPKQQQNEKYQVPQF DQSTIKNIESAKGLDVWDSWPL QNADGTVAEYNGYHVVFALA GSPKDADDTSIYMFYQKVGDN SID\SWKNAGRVF
4277	34645	B	4318	1	1374	
4278	34646	A	4319	1	1293	
4279	34647	A	4320	1	1278	
4280	34648	A	4321	1	1254	MNMNIKKIVKQATVLTFTTALL AGGATQAFAKENNQKAYKETY GVSHITRHDMLQIPKQQQNEKY QVPQFDQSTIKNIESAKGLDVW DSWPLQNADGTVAEYNGYHV VFALAGSPKDADDTSIYMFYQ KVGDNSIDSWKNAGRVFKDSD KFDANDPILKDQTQEWSGSATF TSDGKIRLFYTDYSGKHYGKQS LTTAQVNVSKSDDTLKINGV\N GYYCEES\LFNKA\YYGGGTNFF RKESQKLQQSAKKRDAELANG ALGIIELNNDYTLKKVMKPLITS NTVTDEIERANVFKMNGKWYL FTDSRGSKMTIDGINSNDIYML GYVSNSLTGPYKPLNKTGLVLQ MGLDPNDVTFTYSHFAVPQAK GNNVVITSYMTNRGFFEDKKA TFAPSFLMNIKGNKTSVVKNSIL EQGQLTVN
4281	34649	A	4322	1	726	
4282	34650	A	4323	1	1050	

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4283	34651	A	4324	1	1185	MNMNIKKIVKQATVLTFTTALL AGGATQAFAKENNQKAYKETY GVSHITRHDMLQIPKQQQNEKY QVPQFDQSTIKNIESAKGLDVW DSWPLQNADGTVAEYNGYHV VFALAGSPKDADDTSIYMFYQ KVGDNSIDSWKNAGRVFKDSD KFDANDPILKDQTQEWSGSATF TSDGKIRLFYTDYSGKHYGKQS LTTAQVNVSKSDDTLKINGVED HKTIFDGDGKTYQNVQQFIDEG NYTSGDNHTLRDPHYVEDKGH KYLVFEANTGTENGYQGEESLF NKAYYGGGTNFFRKESQKLQQ SAKKRDAELANGALGIIELNND YT\LKKVMKPLITSN/TVPQAKG NNVVITSYMTNRGFFEDKKATF APSFLMNIKGNKTSVVKNSILE QGQLTVN
4284	34652	B	4325	1	867	
4285	34653	A	4326	1	495	
4286	34654	A	4327	3	1394	GDMNMNIKKIVKQATVLTFTT A/LLAGGATQAFAKENNQKAY KETYGVSHITRHDMLQIPKQQQ NEKYQVPQFDQSTIKNIESAKG LDVWDSWPLQNADGTVAEYN GYHVVFALAGSPKDADDTSIY MFYQKVGDNSIDSWKNAGRVF KDSDKFDANDPILKDQTQEWS GSATFTSDGKIRLFYTDYSGKH YGKQSLTTAQVNVSKSDDTLKI NGVEDHKTIFDGDGKTYQNVQ QFIDEGNYTGDPLEAETAVINH KKRKNSPRIVQSNDLTEAAYSL SRDQKRMLYLFVDQIRKSDGTL QEHDGICEIHVAKYAEIFGLTSA EASKDIRQALKSFAGKEVVFYR PEEDAGDEKGYESFPWFIKRAH SPSRGLYSVHINPYLIPFFIGLQN RFTQFRLSETKEITNPYAMRLY ESLCQYRKPDGSGIVSLKIDWII ERYQLPQSYQRTPDFRRRFLQV CVNEING
4287	34655	B	4328	9	1004	
4288	34656	A	4329	1	768	
4289	34657	A	4330	1	1308	
4290	34658	B	4331	58	753	
4291	34659	B	4332	1	409	
4292	34660	B	4333	1	921	
4293	34661	A	4334	1	1026	
4294	34662	B	4335	1	945	

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4295	34663	A	4336	1	528	MNMNIKKIVKQATVLTFTTALL AGGATQAFAKENNQKAYKETY GVSHITRHDMLQIPKQQQNEKY QVPQFDQSTIKNIESAKGLDVW DSWPLQNADGTVAEYNGYHV VFALAGSPKDADDTSIYMFY/Q KDQTQEWS\GSATFTSDGKIRLF YTDYSGKHYGKQSLDTA\Q*NV VKSG
4296	34664	A	4337	1	1701	
4297	34665	B	4338	97	1449	
4298	34666	A	4339	1	1581	
4299	34667	B	4340	1	1539	
4300	34668	A	4341	87	1078	SLPNLDNAAICSSSSSPTRTR*SL SEGATQ\AFAKEKYPHKHTKKR SGVFHITRHDMLQIPKQQQNEK YQVPQFDQSTIKNIESAKALDV WDSWPLQNADGTVAEYNGYH VVFALAGSPKDADDTSIYMFY QKVGDNSIDSWKNAGRVFKDS DKFDANDPILKDQTQEWSGSA TFTSDGKIRLFYTDYSGKHYGK QSLTTAQVNVSKSDDTLKINGV EDHKTIFDGDGKTYQNVQQFID EGNYTSGDNHTLRDPHYVEDK GHKYRGPLESPSTHQAEFNPTS CVSSLGTLQGFPAPAWLALAHP VHPLKHKSGGSNRLSAAIWGIK RKPAR
4301	34669	A	4342	1	1344	
4302	34670	A	4343	1	1713	
4303	34671	A	4344	3	1918	
4304	34672	A	4345	254	1118	RPPAFAKK*PKAYKET/YGVSHI TRHDMLQIPKQQQNEKYQVPQ FDQSTIKNIESAKGLDVWDSWP LQNADGTVAEYNGYHVVFALA GSPKDADDTSIYMFYQKVGDN SIDSWKNAGRVFKDSDKFDAN DPILKDQTQEWSGSATFTSDGK IRLFYTDYSGKHYGKQSLTTAQ VNVSKSDDTLKINGVEDHKTIF DGDGKTYQNVQQFIDEGNYTS GDNHTLRDPHYVGGTSWEPGV FSVSCVFFGQQEGV/HG*DEFLD FSYWFQGG*ICLYQKAS*QNTT SYKRYTGS

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4305	34673	A	4346	1	1952	MNMNIKKIVKQATVLTFTTALL AGGATQAFAKENNQKAYKETY GVSHITRHDMLQIPKQQQNEKY QVPQFDQSTIKNIESAKGLDVW DSWPLQNADGTVAEYNGYHV VFALAGSPKDADDTSIYMFYQ KVGDNSIDSWKNAGRVFKDSD KFDANDPILKDQTQEWSGSATF TSDGKIRLFYTGSLNSSKTEKY QVPHIDQSTIKNIESAKGLDVW DSWPLQNADGTVAEYNGYHV VFALAGSPKDADDTSIYMFYQ KVGDNSIDSWKNAGRVFKDSD KFDANDPILKDQTQEWSGSATF TSDGKIRLFYTDYSGKHYGKQS LTTAQVNVSKSDDTLKINGVED HKTIFDGDGKTYQNVQQFIDEG NYTSGDNHTLRDPHYVEDKGH KYLVFQDHTGTEEHPQPQ\ERP RTQSFTSAFAERRECIPNVPADT KLSKIKTLRLATSYIAYLMDLL AKDDQNGEAEAFKAEIKKTDV KEEKRKKELASKCLDLEQLGAS VEPTGNLRTKITKEKPRHTGPPE VVVPGCCPHRSRAYKSDKYAH TLTVTASQHAPPPPTHMEGFEL FHLPDLCSPSQDAQTTGRTQMK PDHSPRPSHRVPQAKGNNVVIT SYMTNRGFFEDKKATFAPSFLM NIKGNKTSVVKNSILEQGQLTV
4306	34674	A	4347	1	1029	
4307	34675	A	4348	276	1248	CVWLGCRGYYPKAYKETY\GV SHITRHDMLQIPKQQQNEKYQV PQFDQSTIKNIESAKGLDVWDS WPLQNADGTVAEYNGYHVVF ALAGSPKDADDTSIYMFYQKV GDNSIDSWKNAGRVFKDSDKF DANDPILKDQTQEWSGSATFTS DGKIRLFYTDYSGKHYGKQSLT TAQQLLQLVQFQEVDTDFDFPE EDKKEEFEECLEKFFSTGPARPP TKEKVKRRVLIEPGMPLNHIEY CNHEIMGKNVYYKHRWVAEH YFLLMQYDELQKICYNEFVPSV IFLRYKSPGEAAGTCHLKQRRW VMPEAAAPVGTGSRYPLTGQL
4308	34676	A	4349	1	242	MNSIQIPKQQQNEKYQVPQFDQ STIKYIESPKELDVWDSWPLQN ADGTVAEYNGYHVAFALAG/S PKDADDTSIYMFYQKI
4309	34677	B	4350	1	2198	

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4310	34678	A	4351	1	2796	
4311	34679	A	4352	2047	3531	
4312	34680	A	4353	1	3336	
4313	34681	A	4354	1	1409	MKRAPVIPKHTLNTQPVEDTSL STPAAPMVDSLIARVGVMARG NAITLPVCGRDVKFTLEVLRGD SVEKTSRVWSGNERDQELLTE DALDDLIPSFLLTGQQTPAFGR RVSGVIEIADGSRRRKAAALTE SDYRVLVGELDDEQMAALSRL GGATQAFAKENNQK\AYKETY GVSHITRIIDMLQIPKQQQNEKY QVPQFDQSTIKNIESAKGLDVW DSWPLQNADGTVAEYNGYHV VFALAGSPKDADDTSIYMFYQ KVGDNSIDSWKNAGRVFKDSD KFDANDPILKDQTQEWSGSATF TSDGKIRLFYTDYSGKHYGKQS LTTAQVNVSKSDDTLKINGVED HKTIFDGDGKTYQNVQQFIDGY LLEPDGGALQNFQRYTGIQHVH RIGMAERMWCDRNRERHTVSS SGGNRLPNPGPDRSVRHFPDPR FLCPSCATVTPLHELIANKYLSG KIGAKKLRKLLIKHVD
4314	34682	A	4355	1	2316	
4315	34683	A	4356	93	924	AQTDAAEKSVSIAQLFQACLSIF SSGDV/AGGATQAFAKENNQK AYKETYGVSHITRHDMLQIPKQ QQNEKYQVPQFDQSTIKNIESA KGLDVWDSWPLQNADGTVAE YNGYHVVFALAGSPKDADDTS IYMFYQKVGDNSIDSWKNAGR VFKDSDKFDANDPILKDQTQE WSGSATFTSDGKIRLFYTDYSG KHYGKQSLTTAQVNVSKSNDT LKINGVGKYKTIFDGDGKTYQT VQQFIDEGNYTSGGHHTL\KDP SYNPPLDLSGGNSGYQSQET

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4316	34684	A	4357	1	3118	MNMNIKKIVKQATVLTFTTALL AGGATQAFAKENNQKAYKETY GVSHITRHDMLQIPKQQQNEKY QVPQFDQSTIKNIESAKGLDVW DSWPLQNADGTVAEYNGYHV VFALAGSPKDADDTSIYMFYQ KVGDNSIDSWKNAGRVFKDSD KFDANDPILKDQTQEWSGSATF TSDGKIRLFYTDYSGKHYGKQS LTTAQVNVSKSDDTLKINGVED HKTIFDGDGKTYQNVQQFIDEG NYTSGDNHTL\RDP\HYVENKG HKYLGFETNTGTENGYQGEESL FNKAYYGGGTNFFRKESQKLQ QSAKKRDAELANGALGIIELNN DYTLKKVMKPLITSNTVTDEIE RANVFKMNGKWYLFTDSRGSK MTIDGINSNDIYMLGSDESPND FGNRHLHKERLAVYRWHASFI CSGNTMPIVLVDWSDIREQKRL MVLRASVALHGRSVTLYEKAF PLSEQCSKKAHDQFLADLASIL PSNTTPLIVSDAGFKVPWYKSV EKLGWYWLSRVRGKVQYADL GAENWKPISNLHDMSSSHSKTL GYKRLTKSNPISCQILLYKSRSK GRKNQRSTRTHCHHPSPKIYSA SAKEPWVLATNLPVEIRTPKQL VNIYSKRMQIEETFRDLKSPAY GLGLRHSRTSSSERFDIMLLIAL MLQLTCWLAGVHAQKQ
4317	34685	A	4358	1	1326	
4318	34686	A	4359	2140	4390	
4319	34687	B	4360	1	7271	
4320	34688	A	4361	1	1729	
4321	34689	A	4362	5118	5687	
4322	34690	B	4363	1	4726	
4323	34691	B	4364	1	3688	
4324	34692	A	4365	1	1401	
4325	34693	A	4366	1	1932	
4326	34694	A	4367	1	1407	
4327	34695	A	4368	1	1491	
4328	34696	B	4369	1	855	

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4329	34697	A	4370	137	1014	ASEGKQMLRDFVTTRSALKELL KRALNMARNNQYQPLQKHAK L*RPSML*RNCIN*QPGRDT/TN KKENFRPISLMNIDAKILNKILA NRIQQHIKKLIHNDQVGFIPGM QGWFNIHKSINIIHHIKRTNDKN HMIISIDAEKAFNKIQQPFMLKT LNKLGIDGTYLKIIRAIYDRPTA NVILNGQKLEAFPFKTGTRQGC PLSPLLFNIVLKVLARAIRQETEI KGIQLAKEEVKLSLFADDMIVY LENPIISAQNLLKLISNFSK/VSG YKINVQKSQAFLYTINRQTESQI
4330	34698	A	4371	3	1234	
4331	34699	A	4372	1	2850	MGMGPAKPGMGGNLLVCWLQ RPWEKRSIWAEVYRSSRYSHS WLPLSRKGCDFSGTCRQTLSIL TQPLRQWGLEGIKKPNSWIISEE SVSNGGPPLLIPRQTASGVDLQ QTPTDLQLRVLTVRRKTNKQK GIASTSTKRTSTPKPHLYVTIIK DQSYIKPQRWGKNIAEKLKILKI RVALSLQRNAAPHQQWNKAG RRMSLMSSQKKASEVIESQMN EIKGEEKFREKRVKRNEQSLQEI WDYVKRPDLRLIGVPD
4332	34700	B	4373	16	701	
4333	34701	B	4374	1	3743	
4334	34702	A	4375	227	686	KVMLAEYPVFAQLTLTLPPSSA SWEPSRGPGPRGIRGSCPEWLA SGPG\KAAPGAGVPPPAASFPDP PPRLRAPALAVSRGLRRELPSG LDWTHCLRTLPSLIVQILQQAA LLGLPPAYSDQLQRAGQLHFYS GLIKISLVLTTRLSFWGTTE
4335	34703	A	4376	216	644	VTYSKEKECGEVADSVAKTAL EKDGAPRTGDPRPNLGADPPRS LVSSAGPQAVRPVKPARQFPPQ PPRYSQGPARAAGEEGRGMRPP GAGRRLPGPPLPGPEASHSGQL PLM/PPGPGPRLGSQEPVSLSRY LQTQARMPGPRP

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4336	34704	A	4377	18	1023	QIQHSPLVSPLPSLPPQPLVAEE EPPVA/PWPRRLLPATSTSH/PSH PLTEPVPPT\SGRGCCLWTKRQ QKMCRTTYTSVGRK/CTFPIDS GALRLSDGEMRALQTPTGPQST VEGHTHLQSL/PHHDRVTATPG TEPGLRAAGNRRIFYPGP/VTSQ VQPQLLCGYGNASRTPAALTPG PAPPTQASLPNCGICPHLQMGR PTSPC/PPEGGHPSSSLYISLSPPP PSAPALRLPPPLP\SAPTAPAL/P/ PAAPSAPALRLLRPLPCCSFRPR PAAPSAPAPRLLPPLLVCSFRPC PAAPSAPAGLLLPPLLCCSGLSP RLCCPHSSCSSDPPRLQRKADSS
4337	34705	B	4378	1	984	
4338	34706	A	4379	332	847	VKLLLQDKEICILCQKTVYPME CLVADKQNFHKSCF\RCHHCNS KLSLGNYASLHGQIYCKPHFKP TFQNPKGNYDEGFGHKA\HKD RWNWQKPKADSVDFIPNEEPN MCKNIAENTLVPGDRNEHLDA GNSEGQRNDLRKLGERGKLKV IWPPSKEIPKKTLPFEEELKMSK
4339	34707	A	4380	305	505	GNLERMLNLGMVKQQKLPAIM KTQVLML*AINVPAKPLFPQSG GAVRTTHGGKSRLKETGATSD TE
4340	34708	A	4381	56	260	IVKTQSIDG/MGNLRITEKGLKL EGDS/EFLQPLYAKEIQSRPGLG TQEQSCQTLSSCSSRGQQQHAE
4341	34709	A	4382	137	920	
4342	34710	A	4383	532	1680	LLTTRTSFRSENHRHVGLLLVM TDNTRDKEYFGDESKRENEEKT VEKSIGEKQATLTTHANIITIRH CVKPEPDFSDHLNLLLGRADIT GEEMAAQRSSVEKLANGNIAL VDSLRSRSLEEGDSDPHKRLSG AQDIKTTVEEVIADVVEIARELE LEVEPEDVTEFLQAHEKTLTDV ELFLINEQIKWFLEMKSTPRED AVIIAETITKVLEYDINLVTKQQ QGMRQLTPILKEVLLWVKCHQ TALHATEKPFIKGRINPCGKIHT CLNLRNCGQLLIREEEEEDKEE EEQYEEKEEEEEEEEEEEEEEE EEEEEEEEEEEEEEDEEEEDKE DEEEDKEKEEEEDNKEEEEEED KEKEEEEDKE\EKEDKEEEEDK

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4343	34711	A	4384	3	495	EDTGTFRIY\ESAGAVKKARGF LEFVEDFIQVSKNLIGKVIGKNG KVIQEIVDKSDMVPVRIEGDSE NKLPREDKDDRDSRHQRDSRR CPGGRCRSVSGRRGRGGPRGG KSSISSVPKDPDSNPYSVLDN/T ESDQTADTDASKSHHSTNRHTR SRRRRTDEDAVL
4344	34712	A	4385	1	550	TESERKDELSDWSLAGEDDRDS RHQRDSRRRPGGRGRSVSGGR GRGGPRGGKSSISSVLKDPDSN PYSLLDNTESDQTADTDASESH HSTNRRRRSRRRRTDEDAVLM DGMT\ESDTASVNENGL\AKDV IEEHGPSEKAINGPT\SASG\DDIS KLQRTPGERKRLIP*KKENTQE AAVLNGVS
4345	34713	A	4386	1	2063	MAELTVEVRGSNGAFYKGFIK DVHEDSLTVVFENNWQPERQV PFNEVRLPPPPDIKKEISEGDEV EVYSRANDQEPCGWWLAKVR MMKGEFYVIEYAACDATYNEI VTFERLRPVNQNKTVKKNTFFK CTVDVPEDLREACANENAHKD FKKAVGACRIFYHPETTQLMIL SASEATVKRVNILSDMHLRSIR TKLMLMSRNEEATKHLECTKQ LAAAFHEEFVVREDLMGLAIGT HGSNIQQARKVPGVTAIELDED TGTFRIYGESADAVKKARGFLE FVEDFIQVPRNLVGKVIGKNGK VIQEIVDKSGVVRVRIEGDNEN KLPREDGMVPFVFVGTKESIGN VQVLLEYHIAYLKEVEQLRME RLQIDEQLRQIGMGFRPSSTRGP EKEKGYATDESTVSSVQGSRSY SGRGRGRRGPNYTSGYGTNSEL SNPSETESERKDELSDWSLAGE DDRDSRHQRDSRRRPGGRGRS VSGGRGRGGPRGGKSSISSVQY RSNIHNCSTLKRIFLASDMNIVL KDPDSNPYSLLDNTESDQTADT DASESHHSTNRRRRSRRRRTDE DAVLMDGMTESDTASVNENGL DDSEKKPQRRNRSRRRRFRGQ AE\DRQPAIDFIYKEVEKVVSL WQAKDVIEEHGPSEKAINGPTS ASGDDISKLQRTPGEEKINTLKE

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4346	34714	A	4387	1	1882	CGSNMADVTVEVRGSNGAFYK GFIKDVHEDSLTVVFENNWQPE RQVPFNEVRLPPPPDIKKEISEG DEVEVYSRANDQEPCGWWLA KVRMMKGEFYVIEYAACDATY NEIVTFERLRPVNQNKTVKKNT FFKCTVDVPEDLREACANENA HKDFKKAVGACRIFYHPETTQL MILSASEATVKRVNILSDMHLR SIRTKLMLMSRNEEATKHLECT KQLAAAFHEEFVVREDLMGLA IGTHGSNIQQARKVPGVTAIEL DEDTGTFRIYGESADAVKKAR GFLEFVEDFIQVPRNLVGKVIG KNGKVIQEIVDKSGVVRVRIEG DNENKLPREDGMVPFVFVGTK ESIGNVQVLLEYHIAYLKEVEQ LRMERLQIDEQLRQIGSRSYSG RGRGRRGPNYTSGYGTNSELSN PSETESERKDELSDWSLAGEDN RDSRHQRDSRRRPGGRGRSVSG GRGRGGPR\GGKSSISSVLKDPD SNPYSLLDNT\ESDQTADTDASE SHHSTNRRRR/SIRRRRTD\EDA VLMNGMTESDTASVNENGLVT VADYISRAESQSRQRNLPRETL AKNKKEMAKDVIEEHGPSEKAI NGPTSASGDDISKLQRTPGEEKI NTLKEENTQEAAVLNGVS
4347	34715	A	4388	2	421	PRVRDSDTEDDSEAEHFESFIHP TAMMFTSTINLLQTLCLSAGVH AEIMQSEATKTLCGLL\KSSPNR LVYREQHRSWCTLGFVQSIALT LQVCGALSSLQWITLLMKVVE GHAPFTATSLQRQILAVHLLQA VLPSWDK
4348	34716	A	4389	269	417	DLNCKVGSCFEVYSS*KQGIN*I KLGDSKT*P*LSGPTSENLKNSS LAE
4349	34717	A	4390	1	516	
4350	34718	C	4391	1	1527	

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4351	34719	A	4392	200	1267	TFSKASRGGNPHSMTKAPSDFR KARQTGIPGCSQLGSRYSLEPE QSALRLVCIQKLQESSTTCEDFF CPLCGRAWAVSTPLTDSPSPGH QPAVK*LGLVPFSDTHHPLPFQ VLSTDDTSSSSCSSSCSASSSSP /SLLLLLLFLLLLLLLLMLLLKL FLLLLLFLL/RPPASPPLLPPALS PPL/HCSSSPSAPPASPPPAPPPPP APPPSPPPAPPPSAPSSPAPLPPA PASPPFSCSSSSCSSSCSSSSFSSC SSLSSSAQAEGSLRAPRESSPSL DPSAPQRVKVVPPQAGSGHRA GGALENRPRGKKPWLHFRPGL RSRLPARSLRSRPAPTRWRLRSS GRFTGAATATATART
4352	34720	A	4393	1	2607	MMGHSSAIPLTATPGELKGQSP TKMPDPELGCQGAKSQGCSRN ARHQKARSMPLQDQHLALAIL LELAVQRGTLSQMLSAILLLLQ LWDSRAQETDNERSAQGTSTL LLSLLQTFQSIICSKDTPPSEGN MHLLSGPLSPSESFLRESFFTVQ NCRNNEEVTLICKADLENHNK DGGFWIVIDEKVYDIKDFQTQS LTGNSILAQFAGENPVVALEAA FEFEVTRESMHAFCVGQYLEVR LYALSDAEDGRG\TL*WLQSSIF SG/GLQTSQIHYSYNEEKDEDH CS/SPVGTPASKSR\CSHRWALG DHSQAFLQAIADNNIQDHNVKT HQEQGRSYKEVCTPVIERLRFL SNELRPAVGNDLSIISEFKLLSSL PRWRRIAQKIIRERRKKRIPKKP ESTADEEKIGNEESDLEEACILP HSPINVDKRPIAIKSPKTITSENP LGPSLGSIPQARFLLMMLSMLT LQHSANNLDLLLNSGTLALTQT ALRLIGPSCDNVEEDMNASAQ GVSATVLEATRKETAPVHLPVS GPELAATMKIGTRVMRGVDW KWGDQDGPPPGLGRVIGELGE DGWIRVQWGTGSTNSYRMGK EGKYDLKLAELPAAAQPSAEDS DTEDDSASPNRLVYREQHRSW CMLGFVRSIALTPQVCGALSSP QWITLLMKVMKGHAPFPAASL QRQRWVAVSLPHALVKSGTVP

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4353	34721	A	4394	266	1110	WARGGCARNALASGNAIQGGK CNPGLFPPSPNRLVYREQHRSW CMLGFVRSIALTPQVCGALSSP QWITLLMKVMKGHAPFPAASL QRQLCPE/HTSCPVLKDFCKSVI TDVACSSLISTLLVFWGGLLHT HKEASESWREAKSTSYVAAAR ENEEDAKAEPPTPGIKPSDLVRL IHYQENSMGETAPMIQIISHWV PPTTHGIYGSTIQDEIRVGVSYP GHTDARGFQLLLVSGDFSIPYW SLSSAYTSVNSSFVESLQSNLLK GILLPATIMTDPRTTGHQ
4354	34722	A	4395	1	734	MVQLSGKRILNSPYLELRCHQN MDHLGWVIKKSLNRSEVSWVP GLEFPWGPKPFREVIAGPLLRN NGQSLESSSLEGSHVGVYFSAH WCPPCRSLTRVLVESYRKIKEA GQNF\EIIFVSADRSEESFKQYFS EMPWLAVPYTDEARRSRLNRL YGIQAHLFLTANAEDFDTTVQV NKIILITYRQNENSLSSLKTGET EAQGRLQGSPSNVRGHDPDRH AIPLSVNRWNPSKSSPSPAVWS
4355	34723	A	4396	195	1071	LHEFDSSRDLTSGLGGARTHRR LGGPSDAPRGLPAPPPAPPVRPG /PRSPGPSAGTAR/DAPRPSVQM RAQRPARGSTKDLIETCCAAGQ QWAIDNDECLEIPESGTEDNVC RTAQRHCCVSYLQEKSCMAGV LGAKEGETCGAEDNDSCGISLY KASLTCGLQGRCLNPQQASMG LFSYDVQSSKKINRSIQEKLGG HGVCAATPGGGMRNCGRLRRS GQRRGGTDRCEAVLTGLFTRA LIREQMGDPHPLDHTGQLAKPL EVEKTPARWKYLDTNGEKEEP ELRTQCPSLYED
4356	34724	A	4397	1	520	MMGEKAEKPDTKEKKPKAKK ADAGGKRNCRYSRSAMYSRKT TSRKKYSAAKSKVEKKKKFLA TVTKPVGVDKNSGTQVVKLHK MPRYYPTEDVPLKLLSHG/KKK PFSQHR/RRVVFLKQLV/SGTGP LVLNQVPLRRTHQKFVIATSTKI GSSNVKIAKRLTGAYFKKVWK PKHQE
4357	34725	C	4398	67	243	

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4358	34726	A	4399	1	333	QRSCIENILRAC/VGLPPQNHML LEHKM\DAKRVGPVAATYPML NKKGPVPAATNGCTGDANGHL QEEPPMPTT*GPGHTVSRLFLPA APHDPTLKAPTNNSAATQPSKN KKK
4359	34727	A	4400	587	1013	GAASAGRGPGPRAPGLWGRGP AAAGASLVPTDHVHLSYNHLG NNDGENLSAP/SQFRSKEVSKS NVVDD/MVQSNPVLYTPGEEPD HATRCWPHPSAGPSAADRAVP ARPAGAPATEPHAPGTQNGAP GPSLKRVGPVAATYPI
4360	34728	A	4401	2	334	
4361	34729	B	4402	257	975	
4362	34730	A	4403	30	365	EEAETVLVGQLKQLSSCLAVH KYRPETKQEKKQRLLARAEKK AAGKGDVPTKRPPVLRAGVNT VTTLVENKKAQLV\CRKMGVP YCIIKGKARLGRLVHRKTCTTV AFTQVN
4363	34731	C	4404	62	217	
4364	34732	A	4405	2	69	
4365	34733	A	4406	1	951	GTRPKMPKGKKAKGKKVAPAP AVVKKQEGFRKKW*IPWFEKR P\KNFGIGQDIQPQKRPPPLL*K WPRQYQACSGQRAILYKR\LKV PPAMKPVSPRALD\RQT\ATQLA *AVAHKVQTQRQKQEKKQRL\ LARADEEGCLAKGDVPNERDP PVPSSQEFNPVSPPLVKEQEKLK LVVNWHTDV\DPHPSLVCLPC/ LCPAPVS*KMGGPFTCIIQGKRA RLWDRLVPQERPCTTCPPFT\QV N\SEDKVRLLAKAGLEAIQGPIY N*PDTMEIRPSLGVGNVLG\PKS VARI\AKARNRHKAKETATHTG LNVTLLSFLYYKNN

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4366	34734	A	4407	1	1392	MPDVSEEQKESVCTGSMMREE ESSRKGKVRTAGAKSSSSDRVP RLNQEEVESLNRPITGAEIVAIIN SLPTKKSPAPDGFTAEFYQRIRI QQPIIRIQQPIKKLIQHDKVGFIP GMQGWFNICKSINVIQHINRTK EKNHMIISIDAEKPFDKIQQCFM LKTLNKLGIDGTYLKIIRAIYHK PTANIILNGQKLEAFPLKTGTRQ GCPLSPLLFNIVLEVLARAIRQE KEIKGIQLGKEEVKLSLFADDM IIYLENPTVSAQNLLKLISNFSK VSGYKINVQKSQAFLYTNNRQ TESQIMSELPFTIASKRIKHLGIQ LTRDVKDLFKENYKPLLNEIKE DTKKWKNIPCSWAGRISIMKM AILPKVIYRFNAIPIKLPMTFFTE LEKTTLKFIRNQKRAHIAKSILS QKNKAGGITLPDFKLYYKATV TKTAWYWYQNRDIDQCTRTQP \SEITPHIYNYLIF
4367	34735	A	4408	1	1947	MALRRLSHDVSGALLLANGES TGNSGGSSGSSPSGGATSGSSQ TSISGDVVEACCSVLSMVCADP VYKVYVAAL\QCMLLVTLEDPS SHFTRMRRRLM/AYADEVEIAE AIQLGVEDTLDGQQDSF\CRHL FPTTIWKPQRTVP/LECTIHLEKT GKGLCATKLSASSEDISERLASI SVGPSSSTTTTTTTEQPKPMVQ TKGRPHSQCLNSSPLSHHSQLM FPALSTPSSSTPSVPAGTATDVS KHRLQGFIPCRIPSASPQTQRKF SLQFHRNCPENKDSDKLSPVFT QSRPLPSSNIHRPKPSRPTPGNTS KQGDPSKNSMTLDLNSSSKCD DSFGCSSNSS/NCCYT\SDETVFT PVEEKCRLDVNTELNSSIEDLLE ASMPSSDTTVTFKSEVAVLSPE KAENDDTYKDDVNHNQKCKE KMEAEEEEALAIAMAMSASQD ALPIVPQLQVENGEDIIIIQQDM TFFRHIIPPIQWIYKKESANLLID STGQRLRIADFGAAARLASKGT GAGEFQGQLLGTIAFMAPEVLR GQQYGRSCDVWSVGCAIIEMA CAKPPWNAEKHSNHLALIFKKL LDFANTACDGDKESEVEDVET DSGNSPEDLRKEIMIGLQYQAEI PPYLGEYDGNEKDSPQPKKMT GVQNAKEVLST

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4368	34736	A	4409	1	4485	
4369	34737	A	4410	2	927	IDHMIGHKASLNKFKKIEIISSTL SGHNGIKLEINSKRDLQNHANT RK\LNNLLLNEHWVKNEIKMEI LKFFELNDHNDTTYQNLWDTA KATF\LLRGKFTALNAYIKKTER AQTDILRSHVKELEKQEQTKPK PSRRKEITKIREELNEMETNKK KIQKINETKSRFFEQINKIDRSLA RLAKKRREKIQITSIRNKTGDTT TDTTEIQKIIQGYYEHLYAHKLE NLEEMDKFLEKYNPPSLNQEEL DTLNRTITSNKIEMVIKKLPTKK KSPGPNGFTAEFYQTFK\EELVP ILSILVHKTEKEGTLP
4370	34738	A	4411	405	517	
4371	34739	A	4412	1	1197	MEISELNAKLRSQEKEKQNEIIK LQLEKLQHFQEEKNKEIAILRN TIRDLEQRLSVGKDSHLKRENE QLKISADLIKEKLKSHEQEYKN NIAKLVSEMKIKEEGYKKEISK LYQDMQRKGRIKVTCEWTCSE RKTEGREPGPVREPTGRSQSAE NEGSKTLAEINTKGTQSPAERIN KIDRLLARLTNKRREKVQISSIR NKTGDIRTDTTEKQKFMQGYH EHLYMHKLENLKEMDKFLEIY SPPRLKREDIETLSRPITISDIEM KNLKIPPKLPELINKFSKVSRYK INVHKLVALLYANSDQTDNQIK NSTHFTIVAKK\YLGIYLTKDM KDLHKENSK/PLLKEIIDDTIKW KHIPCSWMSTTNIVKMTILPKTI YKFNAIIIKIPPSFFAERKKQS
4372	34740	A	4413	1	190	MIQRKRASIGAPCAWVRKKEE EEEEEEEEEEEEEEEEEEEE\K KKKKKKKERTTWLWGNPLT
4373	34741	A	4414	303	429	
4374	34742	A	4415	123	252	
4375	34743	A	4416	1	156	
4376	34744	A	4417	3	351	EEEEEEEEEEEEEEEEEEEEE EEEEEEEEEEEEEEEEEEEEE EEEE\KEEEEEEEEEEEGEEEE LGRLHGGSGKVRGLGFTENQQ GSTNRQHQREDNRKSKQKKIN NTKPEATESLIVNGITITAPA
4377	34745	A	4418	1	192	
4378	34746	A	4419	3	259	
4379	34747	A	4420	1	279	
4380	34748	B	4421	1	708	
4381	34749	A	4422	3	269	

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4382	34750	A	4423	1	322	MAGKQGRSEGASSWRLSSVLQ LNSQYFLQGAQQCTFLAATAW KKRKEEEEEEEEEEEEEEEEEE EEEEEEEEEEEE\KKKKKKKK KKKKKKKKKKKKKKKKKKKK KKKKKKKKKKKKKKKKKKKK KKKKKKENPFSCF
4383	34751	B	4424	327	674	
4384	34752	A	4425	494	960	TRFYDHALHLIHRKGSTTVRSP PPLYFIGESKASALLAISLRWSG RSQPRSSVNQIRKAWGFRPRKG TEE/DERSGCPSDALESDDPMA YIHFTAEGEVTFKSILFVPTSAP RGLFDEYGSKKSDYIKLYVRRV FITDDFHDMMPKYLNFVKGVV
4385	34753	A	4426	1	2539	VGGPRGWRCEDPNPGVGGGGG SCDRRGLETHRPHAMRALWVL GLCCVLLTFGSVRADDEVDVD GTVEEDLGKSREGSRTDDEVV QREEEAIQLDGLNASQIRELRE KSEKFAFQAEVNRMMKLIINSL YKNKEIFLRELISNASDALDKIR LISLTDENALSGNEELTVKIKCD KEKNLLHVTDTGVGMTREELV KNLGTIAKSGTSEFLNKMTEAQ EDGQSTSELIGQFGVGFYSAFL VADKVIVTSKHNNDTQHIWES DSNEFSVIADPRGNTLGRGTTIT LVLKEEASDYLELDTIKNLVKK YSQFINFPIYVWSSKTETVEEPM EEEEAAKEEKEESDDEAAVEEE EEEKKPKT\KKVEKTVWDWEL MNDIKPIWQRPSKEVEEDEYKA FYKSFSKESDDPMAYIHFTAEG EVTFK\SILFVPTSAPRG\LFD\DY GSKK\SDYIKLYV\RR\VFITD\DF HDMMPKYLNFVKGVVDSDDL PLNVSRETLQQHKLLKVIRKKL VP*NRWDMIKKI/SLDDKYNDT FW\KEFGYQHSSLVVIEGPLRIR TRLAKLLR\FQSSHHPTD\ITSLD QYVERMKEKQDKIYFMAGSSK KEAESSPFVERLLKKGYEVIYL TEPVDEYCIQALPEFDGKRFQN VAKEGVKFDESEKTKESREAVE KEFEPLLNWMKDKALKDKIEK AVVSQRLTESPCALVASQYGW

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4386	34754	A	4427	2	622	PARAALGILTSHQSGFLKTSTSK IT\STAWKN\KDITMQSTKQYAC LHDLTNKGIGEEIDNEHPWTKP VSSENFT\SP\YVWMLDAEDLA DIEDTVEWRHRNVESLCVMET ASNFSCS\TSGCFSKDIVG\LRTS\ ACWQQHCASPAFAYCG\HSFCC TGTALRTMSSLPESSAMW*KKP ARTRLPRGKDLIYFGSEKSDQE TGTLLLPVSS
4387	34755	A	4428	2	1421	QHCSQKDTAELLRGLSLWNHA EERQKFFKYSVDEKSDKEAEVS EHSTGITHLPPEVMLSIFSYLNP QELCRCSQVSMKWSQLTKTGS LWKHLYPVHWARGDWYSGPA TEL\DT\EPDDEWVKNR\KDESR AFHEWDEDADIDESEESAEESI AISIAQMEKRLLHGLIH\NVLPY VGTSVKTLVLAYSSAVSSKMV RQILELCPNLEHLDLTQTDISDS AFDSWSWLGCCQSLRHLDLSG CEKITDVALEKISRALGNSGHL HQSGFLKTSTSKITSTAWKNKD ITMQSTKQYACLHDLTNKGIGE EIDNEHPWTKPVSSENFTSPYV WMLDAEDLADIEDTVEWRHR NVESLCVMETASNFSCSTSGCF NHRPWSQNEYEQLNYAKQLKE RLEAFTRDFLPHMKEEEEVFQP MLMEYFTYEELKDIKKKVIAQ HCSQKDTAELLRGLSLWNHAE ERQKFFKYSVDEKSDKEAEVS
4388	34756	B	4429	70	348	
4389	34757	A	4430	2	371	
4390	34758	A	4431	1	907	MGHRINIVCKIDAPCARQTRTF HPVVKTVEDCGRYPSVIEFGKY EIQTWYSSPYPQEYARNLAKEG KMGEREMSFVQQLQPMSGRCS LF\RELSSCTYLLNTQPP/AVSIH FLAVWIILLVDGNMSKIYCQNL CLLAKLFLDHKTLYYDVEPFLF YVLTKNDEKGCHLVGYFSKWT VLQGQWQVQGIAHFSRALTYLI CFSFPQEKLCQQKYNVSCIMIM PQHQRQGFGRFLIDFISFPRLTIG ASFTQLRKQSMSNST\EIPLLGD NGKSSPTFHWQSLTSSPNAHFS LEAQLSILGHLFQSP

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4391	34759	A	4432	1	3468	MGKKQNRKTGNSKNQSASPPP KERSSSPATEQSWMENDFDELR EEGFRLSNYSELPEDIQTKGKE VENFEKNLEECITRITNKRNFKP TKIKRDKEGHYIMVKGSIQQEE LTILNIYAPTGAPRFIKQVLSDR QRDLDFHTLIMGDFNTPLSTLD RSTRQKVNKDTQELNSALHQA DLIDIYRTLHSKSTEYRFFSAPH HTYSKIDHLLGSKAFLSKCKRT EIITNYLSDHSAIKLELRIKNLTQ NRSTTWKLNN
4392	34760	A	4433	3	1900	FNKCMTLKFRLKNFSRINKIDTP LARLIKKKREKNRIDTIKNDKG DITSNPTEIQSTIREYYKHLYTN KLENLEEMDKFLDTYTLPRLNQ EEVESLNRPITGSEIMAIINSLPT KKSPGPDGFTAKFYQRYKEELV PFLLKLFQSIEKEGILPNSFYEAS IILIPKPGRDTTKNENFRPISLMN IDAKILNKILANRIQQHIKKLIH HDQVGFIPGMQGWFNIRKSINV IQHISRTKDKNHMIISIDAEKAF DKIQQPFMLKTLNKLG\IKYLGI QLTRDVKDLFKERS/YEPLLNEI KEDTNKWKNIPCSWVGRINIVK MAILPKVIYRFNAIPIKLPMTFF TELEKTTLKFIWNQKRALIAKSI LSQKNKAGGITLPDFKLYYKAT VTKTAWYWYQNRDIDQWNRT EPSEITLHIYNYLIFDKPEKNKQ WGKDSLFNKWCWENWLAICR KLKLDPFLTPYTKINSRWIKDL NVRPKTIKTLEENLGITIQDIGM GKDYMSKTPKAMATKAKIDK WDLIKLKSFCTAKETTIRVNRQ PTKWEKIFATYSSDKGLISRIYN ELKQIYKKKTNNPIKKWVKDM NRHFSKEDIYAAKKHMKKCSP SLAIREMQIKTTMRYHLTPVRM AIIKKSGNN
4393	34761	A	4434	2	1932	

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4394	34762	A	4435	1	2571	MKAEIKMFFETNENKDTTYQN LWNTFKAMCRGKFIALNAHKR KQERSNTDTLTSQLKELKKQEQ THSKPSRRQEITKIRAEMKEIET QKTLQKIKESRTWFFEKINKIDR LLARLTKKKREKNQIDAIKNDK GDITTDPTEIQTTIREYYKHLYA NKLENLEEMDKFLDTYTLPRLN QEEVESLNRPITGSEIEAIINSLP T/KKCPGPDGFTAEFYRRKRG\I LPNSFYEASIILIPKPGTDTTKKE NFRPISLMNIDVKILNKILANRI QQHIKKLIHHDQVGFIPGMQG WFNIRKSINIIQHINRAKDKNH MIISIDAEKAFDKIQQCFMLKTL NKLGIDGTYLKIIRAIYDKPTAN IILNGQKLEVFPLKTGTRQGCPL SPLLFNIVLEVLARAIRQEKEIK GIQLGNEEVKLSLFADDMIVYL ENPIISAPNLLKLINNFSKGSAY KIKVQKSQAFLYTNNRQTESQI MSELPFTIASKRIKYLGIQLTRD VKDLFKENYKPLLKEIKEDTNK WKNIPCSWVGRINIMKMAILPK VIYRFNAILIKLPMTFFTELEKST LKFIWNQKRARIAKSILSQKNK AGGITLPDFKLYYKATVTKTA WYWYQNRDIDQWNGTEPSEIM PHIYNYLIFDKPEKNKQWGKDS LFNKWCWENWLAICRKLKLDP FLTPYTKINSRWIKDLHVRPKTI KTLENLGNTIQDIGMGKDFMSK

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4395	34763	A	4436	1	1965	MTLESEQTFVYAVTATQTGAK EGTRMSKSNVAGQQGDSGEKA LQKTYQKILREKESALEAKYQA MERAATFEHDRDKVKRQFKIF RETKENEIQDLLRAKRELESKL QRLQAQGIQVFDPGESDSDDNC TDVTAAGTQCEYWTGGALGSE PSIGSMIQLQQSFRGPEFAHSSID VEGPFANVNRDDWDIAVASLL QVTPLFSHSLWSNTVRCYLIYT DETQPEMDLFLKDYSPKLKRM CETMGYFFHAVYFPIDVENQYL TVRKWEIEKSSLVILFIHLTLPRI KYLGIQLTRDVKDLFKENYKPL LNEIKEDTNKWKNILCSWTGR NNVMKMATLPKVIYRFNAIPIK LPMTFFTELEKTTLKFIWNQKR AHIAKTILSEKNKAGGIMLPDF KLYFKATVTKAAWYWCQNRD IDQWNRTEASEITPHIYNHLIFD KPDKNKKWGKDSLFNKWCWE NWLAICRKLKLDPFLTPYTKIN SRWIKDLNVRPKTIKTLEENLG NAIQDIGMGKDFMTKTPKAMA TKAKIDKWDLIKLKSFCMAKET PIGVNRQLTEWEKIFAIYPSDKG LISRIYKELKQTYKKKTNNPIEK LAKEMNRHLSKEDIYAANRHK KKCSSSLVIREMQIKTT/MRYHL TPVRMAIIKKSGNNRCWRGCG
4396	34764	A	4437	300	476	PDLSLWLPLTFFPSFQLW*I*QL CVLELLFSRSIFVAFSVFPEFES WPALLGWGSSPG

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4397	34765	A	4438	413	1689	QKLYKPERIKYLGIQLTRDVKD LFKENY/KLNEIKEDTNKRKNIP CSWVGRINILKMAILQKVIYRF NAIPIELPITFFTKLEKTTLRFIW NKKRVHIAKSIPSKKNKAGGIM LPDFKLYYKATITKTAWYLYQ NRDIDQWNRTEALGITPHIYNH LIFDKPDKNKQRGKDSLFNKW CWENWLVICRKLKLDAFLTPY TKINSRWIKDLNIRPKTIKTLEE NLGNTIQGIGMGKDFMTKTPK AMATKAKIDKRDLIKLKSFCTA KETNIRVNRQPIEWEKIFAIYRS DKGLISRIYKELKQIYKKKTNN SIKKWAKDMNRHFSKEDIYAA NRHEKKWSPSLVTREMQIKTIM RYHLTPVRIMTIKMSGNNRCW RGYGEIGMLLHCWWECKLVQ ALWKTVWRFLKDLELEIPFDPV IPLLGIYPKDYT
4398	34766	A	4439	3	2404	
4399	34767	A	4440	1	1572	MLVSFVSLGSLCLQPGSQTLLE KNRTVKPHVSFTLLPALSHVSE KNEAESMNSLIPPPPNLHTPAQ APFPLPTKEQDRSSSPATEQSW TENDFDELTEVGFRRSVITNSSK LKEDVRTHCKEAKNLEKRLHE WLTRINSVEKTLNDLKLKSMA RELHDTCTSFNSRFDQVEERVS AIEDQTNEINNGENGTKLENTL QDIIQENFPNLARQANIQIQEIRR TPQRYSSRKATPRHIIVRFTKVE MKEKVLRAAREKVLEVLARAI SQEKEIKCTQLGKEEVKLSLFA DDMIVCLENPVVSDHNVLKLIS NFSKVSVYKINVQKSHAFLYTN NRQTESQIMSELPFTITTKRIKY LGIQLTRAVKDFFKEKYKPLLN EIKKDTNKWKNIPCSCIGRINIM KMAIVPKVIYGFNAIPIKLPRTF FTELEKTTLKFIWKKKGAKTILS IKNKAGGIMLPDFKLYYKATVT KIAWYWYQNRYINQRNRTETS EITSHIYNHL/IFDKPDKNKKWG KDSLFNKWCWENWL
4400	34768	B	4441	1	1558	

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4401	34769	A	4442	837	4329	TWKGTTDRSTRQKVNKDTQEL NSALHQADLIDIYRTLHPKSTE YTFF/LAPHHTYSKIDHIVGSKA LLSKCKRTEIITNYLSDHSAIKL ELRIKNFTQSRSTTWKLNNLLL NDYWVHNEMNAEIKMFFETNE NKDTTYQNLWDAFKAVCRGK FIALNAHKRKQERSKIDTLTSQL KELEKQEQTHSKASRRQEITKIR AELKEIETQKTLQKINESRSWFF ERITKSDRPLARLIKKKREKNQI DTIKNDKGDIT
4402	34770	A	4443	1	816	MRRDYPVKAFTSRKREQHVQK VPSKKSRQVQRTERRFLETTPD LLYQKEKDLLLISSSKKQPRPGI ERHYMMTQGSIHQEDVAILK/V YTSNKRASKYIQQ/TLLEIKGKI/ AHPQIVGDFNTPTSTIDRTIRQQI SIEFYDTIKQWDLTDTCRTGHPI TEYIFCSGAHLTFTKINHIQGPK RILKRFKRIEIIECVLVLKGCQA KNRKKEEDLQTYWMLNIYGPH YRSGSYAAIHRQETICSGQLSQ ALRDRFAMNAKLLLSLAAHLW VIKLDFM
4403	34771	A	4444	87	307	
4404	34772	A	4445	1	534	MEESRGAKPPPALLPGDATLPP GSLGSARHPPEP/RPVPGP/PPHQ TCPGPSACSSRRPEPRSSPGSPA RAPPAPPPPAAPAPRCEPPLWLL LRVPCPGRSGWSWMTT*I/SERP VQKRARSGPQPRLPPCLLPLSPP TAPDRATAVAT\PPVLGPMSSW SPRRAGGPTRPCTALQALSIPA
4405	34773	A	4446	164	660	YPSGRRLREPADVADAWDGME ESRGAKPPPALLPGDATLPP\AP SGQLGTRPSPPSSRPSPHQTCPG PSACSSRRPEPRSSPGSPARAPP APPPPAAPAPRA/SPRRPLPAPRS ASVPAFSAPPSQWPEVGPSPCA LRRAMPRGPGPPPEPRLVAEPG EDAAPTAGR
4406	34774	A	4447	1	417	

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4407	34775	A	4448	1	1802	MSYPADDYESEAAYDPYAYPS DYDMHTGDPKQDLAYERQYE QQTYQVIPEVIKNFIQYFHKTVS DLIDQKVYELQASRVSSDVIDQ KVYEIQDIYENSWTKLTERFFK NTPWPEAEAIAPQVGNDAVFLI LYKELYYRHIYAKVSGGPSLEQ RFESYYNYCNLFNYILNADGPA PLELPNQWLWDIIDEFIYQFQSF SQYRCKTAKKSEEEIDFLRSNP KIWNVHSVLNVLHSLVDKSNIN RQLEVYTSGGDPESVAGEYGR HSLYKMLGYFSLVGLLRLHSLL GDYYQAIKVLENIELNKKSMYS RVPECQVTTYYYVGFAYLMMR RYQDAIRVFANILLYIQRTKSM FQRTTYKYEMINKQNEQMHAL LAIALTMYPMRIDESIHLQLREK YG\DKMLRMQKGDPQVYEELF SYSCPKFL\SPVVPNYDNVHPN YHKE\PFLQ\QLKGVF**SSSQQ AQLS/TPIRSFLKLYT\TMP\VAK LAGFPGPSQSQEF\RIPGFFVFKQ QDERTSVWTQRVFSAPGW*NF SQASEVDF\YI\DKDMI\HIADTK VA\RRYG\DFFIRQI\HKF\EELNR TLKEGWGQRPWMIFHTHFREP GFECIIGQGSVFC

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4408	34776	A	4449	1	1722	MNIKAKILNKILANRIQQHIKKL IHHDHVSFIPRMQGWFNIHKPIN VIHHINRTNDKNHMIISIDAEKA FDKIQHPFTLKTLNKLDDMTVY LENPIVSAQNLLKLISNFSKVSG YKINVQKSQAFLYTNNRQTESQ IMSELPFTIASKRIKYLGIQLTRD VKDLFKENYKPLLKEIKEDTNK WKNIPCSWVGRINVVKMAILP KVIYRFNAIPIKLPMTFFTELEK TTLKFIWNQKRARIAKSI\LSQK NKAGGITLPDFKLYYKATVTKT AWYWYQNRDIDQWNRTE\PSEI MPHIYNHLTFDKPDKNKQWGK DSLFNKWCWENWLAICRKLKL DPFLTPYTKINSRWIKDLNVRP KTIKTLEENLGNTVQDIGMCKD FMTKTPKAMATKAKIDKWDLI KLKSFCTSKETIIRVNRQPTEWE KMFAIYPSDEGLISRICKE/LFKQ IYKKKNHPIKKWAKDMNRHFS KEDIYVANKHMKKSLSSLVIRE MQIKTTMRHHLTPVRMTIIKKS GNNRFWRGCGETGMLLHCWW ECKLVQPL*KIVW*FLKDLESEI PSDSAIPLGGIHPKAYKSFYY
4409	34777	A	4450	1050	1147	PGEWHGQGSPRCWR*PLPQRC GHLLSCRWRTP
4410	34778	A	4451	1	614	MEELVDEGLVKALGVSNFSHF QIEKLLNKPGLKYKPVTNQNSL GTMQNRAGFPRDEDCLLLQVE CHPYLTQEKLIQYCHSKGITVT AYSPLGSPDRPWAKPEDPSLLE DPKIKEIAAKHKKTAAQVLIRF HIQRNVIVIPKSVTPARIVENIQN TEHYKYCGLCVGPNLEKNLYP VDRM/WKNSCGQFVL*ISSHLE DYPFNAEY
4411	34779	A	4452	2	240	WMELESLSHFQIEKLLN/KPGL KYKPVTNQVNSIQFKGSILEEGI VNMGDDSSMHVSAPEDPPVGQ DVEAEDSDTDDPDPV
4412	34780	A	4453	1	1019	
4413	34781	A	4454	1	2028	

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4414	34782	A	4455	3	1045	DFTSENFSAAWYLIENHSNTSF EQLKMAVTNLKRQANKKSEGS LAYVKGGLSTFLEAQDALSAIH QKLEADGTEKVEGSMTQKLEN VLNRASNTADTLFQ/EKVLGRK DKADST\RNALNVL\QRFKFLFN LPLNIERNIQKGDYDVVINDYE K\AKSLFG\KTEVQVF\KKYYAE V\EPRVEALRELLL\DKLLETPST LHDQKRYIRYLSDLHASGDPA WQCIGAQHKWILQLMHSCKEG YVKDLKGKDFSSNVFQFSGSAL RRVPDTVRVLDSQFSRSALRSV PDTVQVLDSQFSGSALRRVPDT VRVLDGQFSRSALRSVPDTVRV LDKCHCSPAKVVMNAVTIFTG
4415	34783	A	4456	1	440	MQRNLARAFSPGIKKIKMMCL GNSEKDWPKFRGVGEDAGLLA ARECGALLVIRHLINAVRAIVP NKSNNEIILVLQHFDNCVDK\TV QAFMEGSASEVLKEWTVTGKK KLLLQGEEELARLPFITGGSGSC YSSSTLAVEEECRVLA
4416	34784	A	4457	1	276	MEDEMEGLTEAGFRRWVTTNS AELKEHVLTQCKEAKNLDKRL EELLSRITSLERDISDQME/RELC EAYTSINSQINQAEERISEFEDH LAEI
4417	34785	A	4458	3	361	EMVHRKKKAVHRTATADDKK LQFSLKKLEVNNVSGIEEVNMF TNQGTVIHFN\AEMPANSFTITG HAETKQLMEMLPSILNQLGAH CLTSLRRLAEALPKQSVNGKAP LATGEDDDEVPA
4418	34786	A	4459	1	475	
4419	34787	A	4460	57	820	EDGSGGGKFPEGARQGGTGQR RRRKAMRRTGAPAQADSRGRG RARGGCPGGEATLSQPPPRGGT RGQEPQMKETIMNQEKTRHTC RAQ\VRIGGKGTARRKKKVVH RGAAS/ADDKKLQF\SLKK\LGV NNISGIE\EVNM\FTN\QGTSGST FNNP*KFQGISWPANTFHHLQG HAEDKGS*QEMLAQHLKPSLG ADSLTSLRRLAEALPKQSVDGK APLATGEDDDDE\VPDLV\ENF* *RLPRNEANLNLSQLLKIKP
4420	34788	A	4461	1	1527	

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4421	34789	A	4462	8	327	LIWQLTFTKTIKS/CEEYGKIVST KAILDKNTNQCKGMCKGIRTL KSCLCYLINGSSIVEVQKRLAY AGTLEPSLVHQVYSELSYYKLP GTQVVRIIAEVLRMQDSSE
4422	34790	A	4463	2	573	WMEGREKWRGRRKDGRKEGR KEGRKERRREREKGRERK/GKE RKGKERKGKERKGKERKGRER KGTEGKGTEGKGKERKGKEGK GKERKGKERKGKERKGKEGKG KEQKGKERKGKERKGKERKGK ERKGKERKGKEEKGRERKGKE GKGRERKGKEGGKEEGRKERR KEGRKEGKKFSNNGMVEEMQ
4423	34791	B	4464	1	1344	
4424	34792	A	4465	3	373	
4425	34793	A	4466	1	3864	MQWEEAEKDPSGSCVFQRPPV ALVFPLHSKWTLVNSPPSSGDP YVPGRPAQSGQLSLSPAPPYVL PGPGKIKQAGNNPSLTSIYRSEV FCAHRHLHPPQLVCARGHIGSA HLSVDRGSLIWEVLESTVWART NEWSPVTRTVLISALASTHIPQP CESRPPVPPEYEVTVLRSQGTA QLPPWSSSTSWRLTDPSCPKHA AWLTDLASSKGPAAGGTGSFS QPGTLTSTRTNPLKKEKSPEDL KQIKIDLGKFSDN
4426	34794	A	4467	3	415	
4427	34795	A	4468	396	676	LCFPYAERPDLQFLC*DLCARSP YLLQAQKYLQEF*AIPHLDQQT EPPDPSVSFYLLDCTLNCTAQH KTC*KKSIGL*EQNQQTLSSIPY SHT
4428	34796	A	4469	1	858	MEWEDNLPLELGRTVAKLLSD HSQTPLGIQMFLLFSLSLRKSPL VCLSYLFNFRFTLESEVQHLSG AITLTAWPKIPFLGIREAKSPRS ENTRLATILEAGHRHLGTSVSK DHPVTFWRPRRDLQSDLKQIKI DLGKFSDNPDGYIDVLQELGQS FDLTWRDIMLLLNQTLTPNERS ATITAAREFGDLWYISQVVAAV AGLVSEAVKIIQG\LTVWT/SHD VNGILTAKGDLWLSDNHLLKY QALLLEGPVLRLRTCATLNPAT FLPDNEEKIEHNCQQVIAQTYA
4429	34797	A	4470	918	1939	

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4430	34798	A	4471	3	2693	PQVCLTIESQEVNCLLDAGAAF SVLLSCPGQLSSRSVTIRGVLGQ PVTRYFFQPLSCDWGALPFSHA FLIMPESLTPLLEREILVKAGAII HLNIGEGTPICRLLFEEGISPEV WATEGQYGQAKNAHFVQVKL KDSTSFPYQRQYPLRPEAQQRL QKIVKDLKAQGLVKPYSSPCNT PILGVQKPKRQWRLVQDLRIIN EAVFPLYPAIPSPYTLLSQIPEEA EWFTVLDLKDAFFCIPVHPDSQ FLFAFEDPSNPTSQLTWTVLPQ GFRDSPHLFGQALAQDLSQFSY LDTPVLQCMDDLLLAARSETLC HQATQALLNFLTTCGYKVSKP KAQLCSQQVKCLGLKLSKVTR ALSEERIQPILAYPYPKTLKQLR GFLGITGFCRIWIPRYGKIARPL YTLIKETQKANTHLVRWTPEAE AAFHALKKALMQAPVLSLLTG QDFSSYVTKNKQTKKKK\T*IA LRVLALV*GTSLQPVAYLSKKT DVVAKGWPHCLWVMAAIAVLI SKAVKMIQ*RDLTVWTSHDVN GILTAKGDLWLSDNHLLKYQA LLLEGPMLRLCTCAALNLDTFL PHNEEKIEHNCQQVIAQTYATR GDHLEVPLTDPNPNLYTDGRSF VEKGLQKVGYAVVSDNGILES NPLTPGTSAQLAELIALTWALE LGEGKRVNIYTDSKYAYLVLH AHAVIWREREFLTSEGTPIKHQ
4431	34799	C	4472	11	1639	
4432	34800	A	4473	95	2539	
4433	34801	A	4474	345	768	PRGARSTRCLPVERR\CDGLQD CGDGSDEAGCPDLACGRRLGSF YGSFASPDLFGAARGPSDIHCT WLVDTQDSRRVLLQLELRLGY DDYVQVYEGLGERGDRLLQTL SYRSNHRPVSLEAAQGRLTVA YHARARSHPLMNE
4434	34802	A	4475	47	563	RLRFAVFTGAFHALSFLLSFVV LCCTYLKGLKVARFHCKRIDV/ MHHADARAAGGPAPQCAGTLS \EEQKRRRQRATKKISTFIGTFL VCFAPYVITRLVELFSTVPIGSH WGVLSKCLAYSKAASDPFVYS LLRHQYRKSCKEILNRLLHRRSI HSSGLTGDSHSQNILPVSE

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4435	34803	A	4476	1	332	ERGRQEMSAKLRPPAEPPCVPA RISP*RPS*RQ*MERRCPPWRCS PMPC/CFFREHALQVRCGPTSA DCGRDPLFSPHPKPLPHPVPDIG WVATAGAQRSSSPVPSSLFVW
4436	34804	A	4477	297	943	TGSWGGGGADQLRPALTTALM PPDNRFGENTPAAPANGHCAP\ EPDITLVQDHSELPIGAAATMA HEIGHSLGLSHDPDGCCVEAAA ESGGCVMAAAT/GVRGHPFPRV FS/SCSRRQLRAFFRKGGGACLS NAPD/TRTPGAAALCGNGFVEA GEECYCVS\GQECRDLCCFAHN CSLRPGAQCAHGDCCVRCLVR/ CMEGSGSHQLPRLVPGGDSAEI LM
4437	34805	A	4478	1	836	MGPLTFRDVKIEFSLEEWQCLD TAPGNLYRDVMLENYRNLVFL VMCSHFAQDVWPEHSIKDSFQ KVILRTYGKYGHENLQLRKDH KSVDACKVYKGGYNGLNQCLT TTDSKIFQCDKYVKVFHKFPNV NRNKIRHTGKKPFKCKNRGKSF CMLSQLTQHKKIHTREYSYKCE ECGKAFNWSSTLTKHKIIHTGE KPYKCEECGKAFNRSSNLTKH KIIHTGEKPYKCEECG\KAFNRS STLTKHKRIHTEEKPYKCEECG KAFNQFSILNKHKRIHMGR
4438	34806	A	4479	1	588	MLGKVQQQEQTIAKDLVVTKY KMCGGT/DIANRVLRSLVEASS S\GGQDYILKEGDLVKIDLGVH VDGFIANVTHTFVVDVAQGTQ VTGRKGDVIKAAQLCVEAALC LVKPGNQNIQVREAWSKVALS FNCMPIEGMLSHQLKQHVIDGE KNIIQNPTDQQKKDHEKAEFEV HEVYAADVLVSSGEGKAKDAG
4439	34807	A	4480	85	561	LSHCLPLQTTEVGGFGNLLGY WIACSIGCVLSTGMLSHQLKQH VIDGEKTIIQNPTDQQKKDHEK AEFEVHEVYAVDVLVSSGEGK VRRVPELAKRGD*ECSPDQMLL KLLFQAKDAGQRTTIYKRDPSK QYGLKMKTSRAFFSEVERRFD AMPFTLRY

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4440	34808	A	4481	1	1408	GTSAPQPARSQLLALACLPAPL LARAFARPLLEDRGDSDHSLW LGRETEAAAAQGKRGCSGGSR KMSGEDEQQEQTIVD/DSLVVT KYKMGGDIANRVLRSLVEASSS GVSVLSLCEKGDAMIMEETGKI FKKEKEMKKGIAFPTSIS\VNNC VCHFSP/L*KSDQDYILKEGDLV KIDLGVH\VDGFIANVAHTFVV DVAQGTQVTGRK\ADVIKAAH L\CAEAA\LRLVKPGNQNTQVT\ EAWNKVAHSF\NCTPI\EGMLSH SLKQHVIDGEKP*FQNPTDKQK\ RAHEKADFEVH\DVYAVEGLV KPQERARPKDAGQRTTIYKRDP SKQYGLKMKTSRAFFSEVERRF DAMPFTLRAFEDEKKARMGV\ VECAKHEL/VWQPFNVLYSGRE GDFVCPVLNFTVL\LMPNGPML ITSGPFEPDLYKSQMEVQ\DAEL KALLQSSASRKTQKKKKKKAS KTAENATSGETLEENEAGD
4441	34809	A	4482	3	190	
4442	34810	B	4483	1	588	
4443	34811	A	4484	1	1312	MSSKGSVVLAYSGGLDTSCILV WLKEQGYDVIAYLANIGQKED FEEARKKALKLGAKKVFIEDVS REFVEEFIWPAIQSSALYEDRYL LGTFF\ARPCIARKQVEI\AQREG AKYVSHGATGKGNDQVRFELS CYSLAP\QIKVIAPWRMPEFYNR FKGRNDLMEYAK\QHGIPIPVTP KNPWSMDENLMHISYEAGILE NPKNQAPPGLYTKTQDPAKAP NTPDILEIEF\KKGVPVEGGPTF KDG\TTHQTFL\ELF\MYLNEVA GKHGVGPYLTSWENRFHWELK SRGILRRPQAG\TILYHAHLDIE AFTMGGDRAQIPNQGLGFEFVE LGVYRFSGTAPECELVGPCLRQ SPQERVEGKSAGVPSLKGPRCT SLGPEVPHCSLYNE\ELVKHGT CQGDYE\PN*LPPGFIQTSISLKA EGNYHRLPRAKVTAQIRPRVQ
4444	34812	B	4485	47	482	

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4445	34813	A	4486	2328	3435	KTTTLEDNLGNTIQDIGPGKDF MMKIPKANATKIKIDEWDLIKL KSFCTAKATTKRVNKHDESLRS HYE*WGMLTDCVVMRDPNTK RSRGCGFVTYATVEEVDAATN ARPHKVDGKVVEPKRTVSRED SQRPGAHLTVKKIFVGGIKEDT GGFAFVTFDDHDSVDKIVIPKY HTVNGHNCEVRKALSKQEMAS ASSSQRGRSGRGGGFGGNENFG CGGNFSGHGGFGGSHDGGGYG GSGDGYNGFGNDGGYPGGGPG YSGGSRGYGSGGQGCGNQDSG YGRSGSYDSCNKGGRGGFGSG SGSNFGGGGSYNDFGNYNNQY SNFGPMKGGNF/GGRRSGP*GD GGQYFAKPPNHSGYGGSSSSSS
4446	34814	A	4487	1	762	
4447	34815	A	4488	3	333	
4448	34816	A	4489	1	1676	MRDPNTKRSRGFGFVTYATVE EVDAAMNTTPHKVDGRVVEPK RAVSREDSQRPGAHLTVKKIFV GGIKEDTEEHHLRDYFEQYGKI EVIEIMTDRGSGKKRGFAFVTF DDHDSVDKIVIQKYHTVKGHN CEVRKALPKQEMASASSSQRG RRGSGNFGGGRGDGFGGNDNF GRGGNFSGRGGFGGSCGGGGY GGSGDGYNGFGNDGSNF*G\GG SYNDSGNYNNQSSKFEPMKGG NFGGRSSGPYGGGGQYFAKPQ NQAARCVAARWLFRTEARLVF LQKFPPWAVVEVVTVIVAAPA AATATTRDGGGCSRNCNIPEVF PELLGCPNRRGPPGGVREKQQQ TNSKSTRRQEITKTIAELKEIETR KTLQKINESRSWFYEKINKVDR LLDRLIKKKREKSQIDAIKNDIG DIVTDPAEIQTTIKEYYKRLYAN ELENLEEMDKFLATYSLHSLNQ EEVESLNKPVTSSEVEAVTNSL PTKKSPGPDGFTVLLEVLAPAIR QEKEIKHIPIGREEVKLSLFADD VIVYLENPIVSAQNLLKLISNFS

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4449	34817	A	4490	1	1445	MKCLKFINHKEILEASERKQAE SLDFPFKKLRWHLCEGWIEEER DESRKSETIFKDLFKVPVLKETI YYKFYGPPVYQIETVYFMALSP PKSKQFDKTKQNNNNKKTHQF VIVFFKTDEHLSARGRRRRSIVK VSLLPAVIGLKSKFLKKPDQLR KLF\IGGLSFETTDESLRSHFEQ WGTLTDCVVMRDPNTKRSRGF GFVTYAT\VEEVDAAMNARPH KVD\GRVV\EPKRAVSREDSQRP GAHI/TLVKKIFVGGIKEDTEEH HLRDDYFEEIILNSMEKIEV\IEI MT\DRGSGKKRGFAF\VTFDDH DSVDKIVI\QKYHT/VGNGHNCE V\RKALSKQEDG*VLHPAQRG\ RSGSGKLLVVGRGRWFSVGMD NFG\RGGNFSWSVVAFGGT\RG\ GGGYGWQWGMAYNGFGNDG\ SNFGGGG\SYNDFG\NYNNQ\SS NFGPMKGGNFG\GRSSGPYG\G GGQYF\AKPR\NQGGYGGSSSS\
4450	34818	A	4491	134	612	TVLNSMSVILAISTLLKIITGELL QSFGDGLLWNLVIGIRGIDGLSP KVRKVLQLLRLRQIFN/GTFVK LIKVTVNMLRTVEPYIAWGYPN LKSVNELIYKHGYGKISKKRIA LTDNVLIARSLGKYGIICMEDLI YEIYTVGKRFKEANNFLWPFKL
4451	34819	A	4492	1	1983	
4452	34820	A	4493	1	1527	
4453	34821	B	4494	1	2211	
4454	34822	A	4495	1	2478	
4455	34823	A	4496	2	1544	
4456	34824	B	4497	1	2151	
4457	34825	A	4498	1	744	
4458	34826	B	4499	1	2172	

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4459	34827	A	4500	1	2535	MKSGHPEKEQDNSDVQETREIT IRGLLCTALMRHSTGAIAYLGV LSGSASLKLAGVPLRCCEGDKD AGHPLETQTALCERGRGARSLV GNTIMTSQPVPNETIIVLPSNVIN FSQAEKPEPTNQGQDSLKKHLH AEIKVIGVNLIQNVLERGWGKC QEMIYVLGLDICRPFFVSRVSEE GRMGQRGEEDANSLDFPPASLL CLICQEQGVNGESCSPVGMYH REIVPVYEVLSVITGLQIQVFSG KEADSVIKRSIGWGPFFKPRTK DKNHMIISIDAEKAFDKIQQHF MLKTLSKLGIDGTYLKIIRAIYD KPTANIILNGQKLEAFPLKTGTR QGCPLSPLLFNIVLEVLARAIRQ EKEIKGIQLGKEEVKLSLFADD MIVYLENPIVSDQNLLKLISNFS KVSGYKINVQKSQAFLYTNNR QTESQIMSELPFTIASKRIKYLGI QLTRDVKDLFKENYKPLLNEIK EDTNKWKNIPCSWVGRINIVK MAILPKVIYRFNAIPIKLPMTFF TELEKTTLKFIWYQKRARITKSI LSQRNKAGDITLPDFKLYYKAT VNKTAWYWHQNRHIDQWNRT KPSEITLHIYNYLFFDNPDKNKK WGKDSLFNKWCWENWLAICR KLKLDPFLTPYTKINSRWIKDL NIRPKTIKTLEENLGITIQDIGMG KYFMTKTPKAMATKAKIDKW DLIKLKSFCTGKETTIRVNRQPT
4460	34828	B	4501	1	1785	
4461	34829	A	4502	1	1415	
4462	34830	B	4503	1	3262	
4463	34831	A	4504	1	278	

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4464	34832	A	4505	3	2528	ENKDTTYQNLWDAFKA\VCRG KFIALNAHKRKQEKSKIDTLTS QLKELEKQEQTHSKASRRQEIT KIRAELKEIDTQKTLQKINESRS WFFERINKIDRPLARLIKKKREK NQTDTIKNCKGDITTDPTEIQTT IREYYKHLYANKLENLEEMDK FLNTYTLPRLNQEEVESLNRPIT GAEIVAIISSLPT/K/KSPGPDGFT AEFYQRYKEE/LEKEGILPNSFY EASIILIPKPGRDATKKENFRPIS LMNIDAKILNKILAKRIQQHIKK LIHHDQVGFIPGMQGWFNIRKS INVIQHINRTKDKNHMIISIDAE KAFDKIQQRFLLKTLNKLGIDG TYFKIIRAIYDKPTANIILNGQKL EAFPLKTGTRQGCPLSPLLFNIV LEVLARAIRQEKEIKGIQLGKEE VKLSLFADDMIVYLENPIVSAQ NLLKLISNFSKVSGYKINVQKS QAFLYTNNTQTESQIMSELPFTI ASKRIKYLGIQLTRDVKDLFKE NYKPLLKEIKDDTNKWKNIPCS WVGRINIVKMAILPKLPMTFFT ELEK\TTLKFIWNQKRACIAKSI LSQKNKAGGITLPDFKLYYKAT VTKTAWYWYQNRDIDQWNRT EPSEIMPPIYNYLIFDKPEKNKQ WGKDSLFNKWCWENWLAICR KLKLDPFLTPYTKINSRWIKDL NVRPKTIKTLEENLGITIQDIGL GKDFMSKTPKAMATKAKIDK
4465	34833	B	4506	1	5401	
4466	34834	A	4507	1	5271	MNIDAKILNKILPNQIQQHIKKL IHHDQVGFIPGMQGWFNIRKSI NVIQHINRAKDKNHMIILIDAEK SFDKIQQPFMLKTLNKLGIDGT YFKIIRAIYDKPTANIILNGQKLE VFTLKTGTRQGCPLSPLLFNIVL EVLARAIRQEKEIKGIQLGKEEV KLSLFADDMIVYLENPIVSAQN LLKQISNFSKISGYKINVQKSQA FLYTNNRQTESQIMSEIPFTIAL KRIKYLGIQLTRDVKDLFKENY
4467	34835	B	4508	924	3423	
4468	34836	A	4509	525	673	RDSWGTCPVSGAGKVDWPPSS *HHR*HQQWCCGMPHQLSTKE NISIKDHLTKEKRKGGAV*RII

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4469	34837	A	4510	25	1766	GTCQFAAMNVVFAVKQYISKM IEDSGPGMKVLLMDKETTGIVS MVYTQSEILQKEVYLFERIDSQ NREIMKHLKAICFLRPTKENVD YIIQELRRPKYTIYFIYFSNVI\SK SDVEVIGLKLIEQEVVAEVQEF YGDYIAVNPHLFSLNILGCCQG RNWDPAQLSRTTQGLTALLLSL KKCPMIRYQLSSEAAKRLAECV KQVITKEYELFEFRRTEVPPLLL ILDRLDDAITPLLNQWTYQAM VHELLGINNNRIDLSRVPGISKD LREVVLSAENDEFYANNMYLN FAEIGSNIKNLMEDFQKKKPKE QQKLESIGS\MKA\FVENYPQFK KMSGTVSKHVTVVGELSRLVS ERNLLEVSEVEQELACQNDHSS ALQNIKRLLQNPKVTEFDAARL \VMLYALHYERHSSNSLPGLM MDLRNKGVSEKYRKLVSAVVE YGGKRVRGSDLFSPKDAVAITK QFLKGLKGVGNV\YTQLQPF\L H\ETLDHLIKGRLKENLYPYLGP STLRDRPQDIIVFVIGGATYEEA LTVYNLNRTTPGVRIVLGGTTV HNTKSFLEEVLASGLHSRSKES
4470	34838	A	4511	1	1335	MAPVTMMGYRSGKMGILADV QLQVGPPGPWLHLVVIAPVPEC ITGIGIFSSWGSPDVGPLLYDIR AIMWGSLAPAENTWILGNNHR RFLAQLKPRVIMQDFSNVISKS DVKSLAEADEQEVVAEVQQVI TKEYELFEFRRTEVPPLLLILDR CDDAITPLLNQWTYQAMVHEL LGINNNRIDLSRVPGISKDLREV \VSSAEIDEFYANNMYLNFAEIG SNIKNLMEDFQKKKPKEQQKL ESIADMKAFVENYPQFKKMSG\ TVSK\HVTVVG\ELSRL\VSERN LAGRFSEVEARNWAC\QNDHS\ SALQNIKRLLQNPKVTEFDAAR LVML\YA\LHYERHSSNSLP\GL\ MMDLRN\KGVFWRKYSKARVL AVVEYGGKRVRGSDLFSPKDA VAITKQFLKGLKQQEIVNCVLA AANVYIKQLPLSIQPSASLNGCI SLEKKPLVSTQRN
4471	34839	A	4512	1	816	
4472	34840	A	4513	26	257	
4473	34841	A	4514	56	236	

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4474	34842	A	4515	170	373	HSPRGSTASF/CEVSETKNPPIPD TPATREAEGLRSRLAVYSTRDS PCVACSGSYTQAQGSLGRKFQ DP
4475	34843	A	4516	262	358	
4476	34844	A	4517	2298	2556	NHKNPRRKPRQYHSGHRHGQG LHD*NTKSNGTKSNGNKSQN* Q\WDLINLKSFCTAKETTIRVNR QPTEWEKIFTIYPSDKGLISRI
4477	34845	A	4518	801	944	DQEPTNSRHILATQMGPSPITKQ SNPGV**KECGFSCSPRVWRYL VS
4478	34846	B	4519	85	660	
4479	34847	A	4520	693	827	
4480	34848	A	4521	272	339	
4481	34849	C	4522	532	2754	
4482	34850	B	4523	1	519	
4483	34851	B	4524	266	935	
4484	34852	A	4525	1	1584	
4485	34853	A	4526	1	723	GALPNGDRGRRKSRFALYKRP KANGVKPSTVHVISTPQASKAI SCKGQHSISYTLSRNQTVVVEY THDKDTDMFQVGRSTESPIDFV VTDTISGSQNTDEAQITQSTISR FACRIVCDRNEPYTARIFAAGF DSSKNIFLGEKAAKWKNPDGH MDGLTTNGVLVMHPRGGFTEE SQPGVWREISVCGDVYTLRETR SAQQRGKLGLQTGDMAENT/T VHALPSNCMVWRRSQTRQQIS
4486	34854	A	4527	1	335	
4487	34855	A	4528	328	871	DCGGGRARTAIFAGAARAADN KKCAGARRALGRARGCSATAR PRRRRRRPRGLAPPRPARPPPG GMSYKPNLAAHMPAAALNAA GSVHSPSTSMATSSQYRQLLSD YGPPSLGYTQGTGNSQVPQSKY AELLAIIEELGKEIRPTYAGSKSS \MERL\KRGIIHARGLVRECLAE TERNARS
4488	34856	A	4529	1	653	MAGPAESSPQGAHPNSPFALQH HSSLTVKPLHRQNVIQHQVAG QENRRGHQAGSSTSPQPLEALK RPNLRAPFHSQSRRILIPPAGNP TPGAAAPADPSTQRRDRWGCA LPMPRVAAGSAHHQQAGPTAA AQHRTPVALFSPPLSLVYGQQQ RKESETPTVPTPPARARGWTET GVEHVPAYNRTRAPEKCDI/SV PSPHSSPDAETSHPRHISPCPG

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4489	34857	A	4530	3	432	NSRVDDFVAAQDAKGKKVAP APAVVKKQEAKKVVNPLFEKR PKNFGIGQ\QRLLARAEKKAAG KGDVPTKRPPVLRAGVNTVTT LVENKKAQLVVIAHDVDPIELV VFLPALCRKMGVPYCIIKGKAR LGRLVHRKTCTTVAFT
4490	34858	A	4531	1	2073	MKPCAHSWNAELSRNIIRHSFN LVMVAASQVAVSQLLGSYEILL LVSIELMFCFGLGYFFIPMQEW PNTYGERVFVDVESSVFKWNH KCLHKTEAERDYTKKRLKLCG HKPGNAVGQQKLEEARNRFFT RAPGGSAALPTLRFQPSDTDFR LLASRTILTFETKNPSELAERLR SVCGNQSNAYARLLEYRLNAL RGLWNAQRQLALEEQHERESS GDEETLALLKRQGLLQQPEQAP FTSRMGLLLVFPLIQSQSRTDPS LCNITAEVLLNCLRDCQPLSLT KEPADCLNGIETLLCSWLEETS DTGRHIPHKQKENAAAALVAL ACARGFVYCRNEELEPGWVAF GSGSLLHRPVSFDNKPHSLFQVI DQNTLQVCQVVPMPANHLPIG STMSTVHLSSDGTYFYWIWSPA SLNEKTPKGHSVFMDIFELVTL KGKKAKGKKVAPAPAVVKKQ EAKKVVNSLFEKR\DIQPKRELT YFVKW/PRYVRLQQQRAILYKQ LKVPPAINQFTQALNCQTVTQL LKLAHKYRPETKQEKKQRLLA QAEKKAAGKGGVPTKRPPALR AGVNTITTLVENKKAQLVVIAH DVDSIELVVFLPALCCKMGVPY CIIKGKARLGRLVHRKTCTTVA FTQVNLEDKGALAKLVEGIRTN DNDRYDEICCHWGGNILGPKS VACIAKLEKAKAKELATKLG
4491	34859	A	4532	1	2565	
4492	34860	A	4533	1	644	MPKGKKAKEKKVAPAPAVVK KQEAKKVVNPLFEKRPKNFGT GQDIQPKRDLTHFVKWPCYIRL QQQRTILYKWLKVPPEINQFTQ APDSQTATLLLKLAH/KYRPET NQEKKQRLLARAKKKAAGKG DIP\TKSPPVLRAGVNTITTLVE NKKAQLVVIAHDVDPIKLVVFL PVLCHK/MGVPYCIIKGKARLG HLVHRKTCTTVTFTQVNSEDK

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4493	34861	A	4534	1	931	KSIQKGLKMCLSSSLLPPSKMP KGKKAKGKKVAPAPAVVKKQ EAKKVVNPLFEKRP\KNFGIGQ DIQP\KRDFTRFVKWPRLLSGC MR\KRAILYKAG*KLPPA\INQF HPGPWDPANKLLQLL*AWAHK \YRP\ETKAKRKKQRL\LARA\E KKAA\GKGDVPNERDPPV\LRA\ GVNTVTHLWWRNKKAPAWVV IATRRWIPFEL\VVFLPAL\CREK WGSPYCIIKGKARLGR\LVH\RR PCT\TVGFHTR*NSKDKRRLLA* AGLEAIRTQFTIDQIRWRSGRH\ WG\GNVLG\PKSVARIRQASKR QRLKELATKLG
4494	34862	A	4535	3	227	
4495	34863	A	4536	1	338	
4496	34864	A	4537	1	352	
4497	34865	A	4538	2	368	
4498	34866	A	4539	3	468	
4499	34867	A	4540	2	790	PRGRNRRRKTFQERRMTLNESP EKIGKWIECYGHPPASKLVEIYI HTVFVEDKLSICIRSFNKKADGS WRMTVDYCKLNQVVTAIAAAI PDVVSLLEQINTSPDTWYAAID LANALFSIPVHKGYINSLALCH NVIWRELDCFSLPRDTTLVHYI DDIMLIGSSVQEVENKLDLLVK DKLLHLAPPTTKEEVQHMVGL FGFWRQHIPHLGVLHQPIYRVI RKAA/SFEWGPEQEKALQQVQ AAVGGKQSENNLGHQRSPGLW
4500	34868	B	4541	179	1219	
4501	34869	A	4542	1706	2517	THLLVPGMQPLTWQMPFSPFLS ISPTRSNLPSAATPVIAQWA/HE QSGHGGRDGGYTWAQQHGLA FTNTDLATVNAKIGFAYPVCDA SAKTTIRGLLECLIRCDGIPHSIA SDQARIHRSRNQEVEVEVAPLT ITPSDPLAKFLLSVPVTLRSAGL EVLVPGEGMLPPGNTRTIPLNW KLRLPPGHFGLLLTLSQEAKNG VTVLAGVIDLDYQDEISLLLHN GGKKEYARNTGDPLGRLLVLP CPVIKINGKLQQPNPGGTTNGS DPSGMKV

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4502	34870	A	4543	3	367	DLWPFTRVTVH/WGKANDQTF QGLLDTGSELTLIPGYPKRHCC PPVKVRVYGGQTDGSWRMTV GYHKLNQVVTPIAAAVPDVVS LLEQINTTPAIKWVVHSSIPSSN GSGVYVIRLEQVLKAQ
4503	34871	A	4544	2	541	
4504	34872	B	4545	1	681	
4505	34873	A	4546	2	1091	PRGRNRRRKTFQERRMTLNESP EKIGKWIECYGHPPASKLVEIYI HTVFVEDKLSICIRSFNKKADGS WRMTVDYCKLNQVVTAIAAAI PDVVSLLEQINTSPDTWYAAID LANALFSIPVHKGYINSLALCH NVIWRELDCFSLPRDTTLVHYI DDIMLIGSIKFLGVQWCGACRD IPSKDPADPMVLEVSVADRDAV WSIWQALIDESQQRPLGFWSKS LPSSADNYSPFERQLLAYYWAL VETERSTMGHQVTMLPELPVM NWVLSDPSSHK/ANGLAGWSG TGKKHDWKIGDKEIWRRGMW MDLSEWSK/D/VKIFVSHVSAH QRVTSAEEEFNNQVDRMTRSM DTTQPLYPTTPVIAQWAHE
4506	34874	A	4547	1	1236	
4507	34875	A	4548	1	1467	GEKGNDQTFRKLLDTGSELMLI PLRVVIPTTSLFNSPIWPVQKTD GSGRMRVDYHKLNQVMTPTA AAVPDVVSLFEPINTFLGTWYA AIDLANALFSIPVCKAHQKQFA FSWQGQQYTFTVLPQRYINCLA LCHNLIQRDLDHFLLPQGITLV HYIDSGPFIK*PEAASFEWGPEQ EKALQQVQAAVQAALSIGPYD PADPMVLEVSVADGDAVWSL WQAPKGESQWRPLGFWSKALP SSTDNYSSSDVQLYTDSWAVA SSLAG*SGTWKKHDWKIGDKEI WGRGMWMDLSEWSKTGKIFV SHVNAHQLVTSAEEDFNNQVD RMTRSVDTTQPLSPATPVVAQ WAHEQSGHGGRNEGYAWTQQ HGLPLTKADLTTATAECPICQQ QRPTLRPRYGTTSQGDQPATC WQVDYIEPLPSWKRQRFLLTGI NTHSGYGFAYPPCNASAKTTIH GLIACLIHCHGIPHSIASLYRER GTHFTDKEVQQWAHAH

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4508	34876	A	4549	2	1602	NLSPILPQDLWPFTRVTVHWGK GNDQTFQGLQDTGSELMLIPGD PKRHCSPPVKVGSYGGQVINGV LAQVRLTVGTVGPRTHPVVISP VPECIIDIDILNSWQNPHIDSLTG RVKAIMVGKAKWKPFEPLLPIK IVNQKQYRIPGGIAEISATIKDL KDAGVVIPITLPFNSPFWPVKKT DGSWRMKVVYCKLNQVVTPIT AAVPDV/VVSLLEQINTSPGTW YAAIDLANAIFSIPVHKAHQKQ FAFSWQGHQNTFTVFTILLHIH KVGHAQQHSIIKWKWYIHDGA RAGSEGTSKLNEEVPQMPMVT TSAALPSLPRPAPMASWGVLY DQLTEEEKTRAWFTDGSARYA GTTQKWTAAALQPLSRTSLKG SGEGKSSQWAELQAVHLVVHF SWKDKWPDVRLYIDSWAVAN GLAGWSGTWKKIIDWKIGDKEI WGRGMWMDLSEWPKPVKIFG SHVSAHQWVISAEEDFNNQVD KMTCSVDITQPLSPATPVITQW AHKQSGHGGRDGGYTWAQQH GLPLTKTGLAMATAECPI

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4509	34877	A	4550	1	1891	MLSSTQNAGGSYQRVRGALDT QEWKWGEVSPRTLNVDGRAL VSVANTHGTDRPAYTLNPQSR DQRSGVITLGYKRPLEREDLFE LKESDSFCTACPIFEKQWRKEV LRNQERQKVKALNKLDEALCP GIILTQSTDSNANLFQKQPHRHT QTSGRWQIIIFCEHSSDFGWNG YGYAVALLVVVFLQTLILQQY QRFNMLTSAKVKTAVNGLIYK KLGWSGKVSWLILHDVGHGIM EGYIAWGKGSDVRITWEKKST EMRTRPAQKMALLLSNVSRQK FSTGEIINLMSATHGLDSKPQSP LVCPFSNPNGRISPLARAGLAD HYRVTHLQILKLYAWEPSYKN KIIKIRDQELEFQKSARYLTVFS MLTLTCIPFLTKISLGRLEDFLN TEELLPQSIETNYTGDHAIGFTD ASFSWDKTGMPVLKESIRIRIEQ VLNQLSLFETVDYPGSVAYVSQ QAWIQNCILQENILFGSIMKKEF YEQVLEACALLPDLEQLPKGD QTEIGERAVNISGGQQHRVSLA RAVYSGADVYLLDDPLSAIDV HVGKQLFEKVIGSLGLLKNRTH ILVTHNLTLLPQMNLIVVMKSG RIAQMGIYQELLCKTKNLTN\FT KSSVNKKKVGEWEESGRGS
4510	34878	A	4551	2	542	LTSAKVKTAVNGLIYKKVSLAT LCVYFLLDERIILTAPKVFTSMS LFNILRIPLFELPSVISAVVQTKI SLGRLEDFLNTEELLPQSIETNY TGDHAIGFTDASFSWDKTGMP VL/NRGSEAYVSQQAWIQNCIL QENILFGSIMKKEFYEQVLEAC ALLPDLEQLPKGDQTEIGERVR
4511	34879	A	4552	1	667	IETNYTGDHAIGFTDASFSWDK TGMPVLKESSVAYVSQQAWIQ NCILQENILFGSIMKKEFYEQVL EACALLPDLEQLPKGDQTEIGE R/GKETAVNISGGQQHRVSLAR AVYSGADVYLLDDPLSAIDVH VGKQLFEKVIGSLGLLKNRTSH SVCHYTLLAVPHLLEVQILTGN FIQSLGFNYHEYANNSNAYIVN LDLFPGFQTCVYKLLSPIRCLIC
4512	34880	A	4553	201	336	QQTPGKAVHAPFIADQSLT*EL VSVFPQFQLFPYRR*DSHSGKS
4513	34881	A	4554	3	515	

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4514	34882	A	4555	1	852	MPCTTSGLDKVPTSKKALTRY GYGSLTLDFSGSIIPCKMCLSPS TRIVRPSQPRGTEDPDETGDTEF VNSDESFLLEGTASPSPVVAVSP PRPMLPSAFPPLSEDINPVLPEA TVLASPEVVAKQTHVDSPRKPL STFLFASRPVTKLKSRQTPGGE VDSVTCEEKTDGPWRKTVDYC KLNQVVTPIAALVPDMVSLLV QINTSSDTSYAAIDLAKAFFSIP VYKAHQKQFIFSWQAQQYTFT VLPQGYIISPALCHNLIRR/DLD HFLLPQDITLVHYIDDIRL
4515	34883	B	4556	288	327	
4516	34884	A	4557	51	598	LFGGCHTSGGLAVRVPRMPRG SRSRTSRMAPS\ASRAPLK*ELE PRQAQVAQPPA\AAPPSAVGSS\ AAAPRQPG/LFMAQMATTAAG VA\VGFCCGGHTLGHGI\TGGLS VGGKLIA*ALRRP*HQFNQGSF RGTQAKHSKQQPALPLLWRIKT SFREVVPPEPRVTIQGFCGGFPM RLLETVPDL
4517	34885	A	4558	1	10434	MTVIRSGIAYILHLKSYDVNIQT GSNACNQPTHPNGDCSHFCFPV PNFQRVCGCPYGMRLASNHLT CEGDPTNEPPTEQCGLFSFPCK NGRCVPNYYLCDGVDDCHDNS DEQLCGTLNNTCSSSAFTCGHG ECIPAHWRCDKRNDCVDGSDE HNCPTHAPASCLDTQYTCDNH QCISKNWVCDTDNDCGDGSDE KNCILNCTASQFKCASGDKCIG VTNRCDGVFDCSDNSDEAGCP TRPPGMCHSDEFQCQEDG
4518	34886	A	4559	24	849	ATGRCCCGLAPGFPLCWVLYP GGRGSA\CPEPHVLRTGSPLQRE QRTNGRTDLSSLLPNLNFDSPP RCKHKNQLAITLRKRIRKLATS LFSSTIFRISGTSVIISAPGAGLPL PALFPTRCQPKFSRSIDPTGKAV QTADIRLSARATLWLGGSIEESP VLCSTLRLLLRRLPPPLTWTSPN RPTQPCTAQTQTNQSVGIAAPS AIRVIYPESVVLNAVIYLPGDPE VSGLPRAFKRRFSVEVRLDCGT FKLLLVYCTHPGDKKVNTCKT GALVAF
4519	34887	C	4560	192	449	
4520	34888	A	4561	1	786	
4521	34889	A	4562	3	14073	

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4522	34890	B	4563	58	1282	
4523	34891	B	4564	1	684	
4524	34892	A	4565	1	1356	MGRKYTLKWEFEEGFTEKKEL KKVTSEGYITPVEIYDYRQYCY ALQRPIATTQIDDVRDGHTTRL AKLEKQEQTHSKASRRQEIIKIR AEPKEIETQKTLQKINESRSWFF EKINKIDRLLARLIKKKREKNQI DAIKNDKGDITTNPTEIQTTIRE YYKHLYANKLENLEEMDKFLH TYILPRLNQEEVESLNRPITGSEI EAIINSLPTKKSPGPDGFTADFY Q\MLEVLARAIMQEKEIKGIQL GKEEVKLSLFADYMIVYLENAI ISAQNLLKLI/SNFSKVSGYKINV QKSQAFLYINNRQTESQIMSER PFTIASKRIKYLGIQLTRDVKNL FKENYKPLLNEIKEDTNKWKKI PCSWVGRINIVKMAILPKVIYRF NAIPIKLPMTFFTELEKTTLKFI WNQKRACITKSILSQKNKAGGI MLPEFKLY/YQGSSTQTAWYW
4525	34893	A	4566	1	1102	MANCDINRKDEKGGKEKKDRS KSKSLMDTLKRQLSAKQKPKG KAGKPSGSSADEDTFSSSSAPIV FKAVRAQRPIR/STSLRSHHCSP MPWPLRPTNSEETCIKME\PSPP LNGVRKDFHDLQSETACQEQA NSLKSSASQNGDLYLRLDEHVP VVIGLLPQDYIQYTVPLDEGMC PLEGSSSYCLDSSSTMEVSVVPS QVGGRSFPEDESQADQNLVVA PEIFVDQSMNGLLTGTTGVMLQ SPRVGPHHVPPLSPLLPPMQNN QIQRNFSGLTGTEAHMAESMLC HLNFDFNSAPGVARVYVSVQSS GPMVVTSLTEELKR\LAKQGWL WPPLKSVRRCVLARRSLYTKQL NQEEGTELNLGSSCLLC
4526	34894	A	4567	364	661	PFHFTCFSCKVYFADPGSAARS VPGSPSAVCAQCILCTGHCAVC PGLGEHHSSGRTLMKTKLHSK KLKPCYLLC*SKN*KTQGGSPK S*NVNKYLVTLI
4527	34895	A	4568	53	470	CISIIILPGPSAKTLSPVLSLSSPY TASFQPTFVRTFSHQTTYLSLGS VPVAQLKCSAGQQRGELLCRR GVWGSWISVSHFTEIATLPAAC LEDGE\DFNLGGILDSSKYL*SIQ KTNTHRIVDGKVVSETNITDVL

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4528	34896	A	4569	1	1635	MGWTCKILFLVAAATGAHFLV QLVQSGAEVKKPGASVKVSCK ASGYTFTYCYLHWREPVSFICG RCILLTLLLGDCLWGEGAWTQ GDVLQPSDRASFLAMGVNTTG QQVGDLSGDFPNSVGKACKCR EFHTLTPLAHTSSTTHETFPGMS HIALELSQGSSLLQCLEAQTQG QRQELTVSANEQPESRGHGCVL LCETQSEGKSVRAQAQTSLKGS QKRLGGARTLCTGLSPGQRKQ ERSKIDTLTSQLKELEKQEQTYS KASRRQEITKIRAELKEIETQKT LQKINESRSWFFEKIYKIDRPLA RLIKKKREKNQIDAIKNGKGDI TTDPTEIQTTLRQYYKHLYANK LENLEGMDKFLDAYTLPRLNQ EEVESLNRPITGPEIEAIIN/STPT KKSPGPDRFTAEFYQ\RSDVLA RAIRQKKEIKCIQLGKEEVKLSL FADDMIVYLEIPIISAQNLLKLIS NFSKVSGYKISVQKSQAFLYTN NRQTESQIMSELPFTIASKRIKY LGIQLTKDVKDLFKDNCKPLLN EIKEDTNKWKNIPCS
4529	34897	B	4570	1	429	
4530	34898	A	4571	1	897	MDLNYTLEQMDLTDIYRTFHPT TTEYTFYSTGHGTFSKTDDVIG HKMSLDKFKKIEMISNTVSDHS GIKLEINSERNLENHANTWKLN NLLLNECWVKNKMKMEIKKLF ELNDNNDTTYHNLWDRAKVVI RGKCIALNTYIKKSERAQTDNL RIKNKNHMIISIDAEKAFDKIQH PFMIKTLSKISIRGTYLNLIKDIY DKPTANIMLNGEKLKAFTLRTG T\RMNQGCPLPSLLFNI/VLEVL ARAIRQEKEIKGIQIGKEEVKVS LFADYVIVYFENPTDSSRKLLEL IKEFSSFWIQD
4531	34899	A	4572	1	1461	
4532	34900	A	4573	49	365	
4533	34901	A	4574	45	534	VCHLEPGERCGPSRGCRAVGV QTEKMQTAGALFISPALIRCCT RGLIRPVSASFLNSPVNSSKQPS YSNFPLQVARREFQTSVVSRDI DTAAKFIG\AGSATVGVADSGA GIGAVFGSLIIVYARKLSLKQQL LFYAILGF\ALSEGM\GLFCLMV AFLILFAM

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4534	34902	A	4575	98	624	DWYSRSHPKELWEGSKKKSIN HSACSLQAHGGPISTSLNPHSKP RGRVSPPPGKRQQECRARPGRS PELAGPPPANVQETSQKNACAS RLSEPPGEGP\EPAAHPQPHRGS SSGPCSRGGYRQPLFPGPAASG VPASGSV/RSRIPGAPQGVALAR RGPQGSPSPAPRFFPATERQS
4535	34903	B	4576	1	604	
4536	34904	A	4577	3	331	LAPAPSAAWRTGLKALTPSST WMLCASE\HHVGSGCVGDHLA GCRQEKTLPCQR\YCVFCRRRR ARSLQAQCGFSLTPALELLPVPF LKLLCPGPPRRRRICRILPGAGL
4537	34905	A	4578	1	871	
4538	34906	A	4579	3	510	GPPSRVDDFVAAAAAAVAPVV LYACPRHSPIPPWSIRGRRVVVT GFGPFGEHTVNANWIAVQELE KLGLGDSVDLHVYEIPVEYQTV QRLIPALWEKHSPQL\VVHVGV SGMATTVTLEKCGHNKGYKGL DNCRFCPGSQCCVEDGPESIDSI IDMDAVCKRVTTLGQCI
4539	34907	A	4580	1	285	MAPGALPALGEEEGPGASGLSA ELGHLSAGSRAFRETSVDSALD TPFPAGTFVRLEFKLRQTE\SGR RKDWKKPKCKVQPERRKQKCL TCVKLEC
4540	34908	B	4581	1	228	
4541	34909	A	4582	1	697	MGLERPVDRVMWLPGALWNS AVVSAPVGEEWALAGTGNQGL QDIQGMHCPEEGISQIHGRDHR NAKDSHTGVWCSCTLGIISTIIIR PKCRFSIDRSDSDYLPTSSCRRD PGGAEPCQDRPRVEQLCSVLAN RSGPLAKCHWYESPVSYTQVC VSDLCQYGTGNRMLCTMLEAY VQLCALRCALPARVASQPGMQ LRVACPANSYYDSCGPPFPATC ASLNSSAPCTLQCTVSCFCLEGF ALEAG\SSVPHACCGCHLQGRY I/APGPWPSATGMRAPCPTRRC VSLTSASMARATACCAPCWRP TSNSAPCAARCLPAWRASLGCS YVWRVQPTATMTPVGHPSRPP VLASTPPRPAPSSAQ
4542	34910	B	4583	1	208	
4543	34911	A	4584	2	230	

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4544	34912	A	4585	106	669	GCGCVLLPGGVGAPGHSPEGP VPPRDARQLRTCGLAGTLHLST SCGHPTGAWRGALGSQWNGH NPVQDHLQEAQPWFLEFDRG* RCFWRMATSFPRYPTWDDY*R LPCCRCLPQCKKPAETTGCLPIS GEKTHGGVGDLLGEAPARLRQ WASQRQPATDLPA*ASRGRPA* GKDTHRACVAGEAAQDA
4545	34913	A	4586	2	597	TPKGGIRLGLAKLGCPTAWINP YGRGMPLAHSVLSSGARVLVV DPDLRESLEEILPKLQAENIRCF YLSHTSPTPGVGALGAALDAAP SHPVPADLRAGITWRSPALFIYT SGTTGLPKPAILTHERVLQMSK MLALSGATADDVV\YTEVLPLY HVMGLVVGILGCLDLGTSLAS YGLRVYFILWSVLGPSRRTLCL
4546	34914	A	4587	9	573	EEEERKKKKK\KKKEEEEGEEE GGGMGEKKKKEEEEEGEEEGE KEREKER\EKERKKKKEERKEK ERERKKKRERKKEKERERKEG EGERERKSTECTSSSYI/IKKLVV KQPQAAPSGEIPEEGIAVLGGDS SMPVIVPEDLPVGQDVEVEDSD INDPDSLILVSSQAGGGGVITAY CNLEHLGSSDPPT
4547	34915	A	4588	1	297	
4548	34916	A	4589	114	752	DGSAAPRATSDSFTYTVCVSEF PVDDFMELGRSIPDTQL/DAVIE SQKANQCAVLIYT/SGTTGIPKG VMLSHDNITWIAGAVTKDFK/P TDKHETVVSYLPLSHI/AAQMM DIWVPIKIGAL/IYFAQADALKV RLSKDLGSDFILLGSPVGLRPST KRLPVLSKLGHTYRRVVWVEE SSGPHTISNQNNYRLQGPMMK LKRHFVAQKYKKQIDHMYH
4549	34917	A	4590	1	837	MVTQKLPNAQENLKHAERQAA GCCPGRSHIFQHVGPGASESLR GEGCSTHPEAQGAQERCEQWK KDQHWCLASHTDVTQQWGRH IVQEGGTHRGPSAVLSLRTALD EG/ARGGCSHPITAQLPLQLRHL PRPPPAPAR\PSPAPPAATSPPT\P PPAPAR\SSPAPPAATSPPTASSG ACAALPQLPLQLRHLPRPPPAP AR\SSPAPPAAMSPP\RPPAPARP RLRRSTACATALRPGERGSAAA QPGARSETSFCRLG/AAAAVLD PAFISSQALACPVVGVI

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4550	34918	A	4591	3	377	
4551	34919	B	4592	1	1632	
4552	34920	A	4593	1	1224	MDGTNRFYLYVWETERQQDV EHVARCILCYDKCRPDPECPAG TPGPQEVDVDLVFVVDSSYGV DADVYRGSLSLADAALEDLEV AEQPGASHRGARVALVTHTTP NF\GRGFHLTTYGNRKQMQRH VREASARPLQGTAPPGHALEW TLENVLLAAPRPRKAQVLFAIV ASETSSWDREKLWTLSLEAKC KGITLFVLALGPGVGTHELAEL AELVSAPSEQHLLRLQGVSEPE VNYAQGFTRAFLNLLKSEQSPG TGAPWVEWGEGFTEPGIWACR WTNQYPPPELTEECGGLHRGD TVLQLVTPVNRFMYAAKENSL KRKTKANFHLAVELELDESYFR AYYEGTLYEVSALPLQRSNELL QKWSLFHGSNGRRVSGSHPEV ALQQGGTGLPAVLVWQLWRQ
4553	34921	A	4594	266	556	HKVQQICYRLRLVSQILFSINQT LAERQIVTFTVYPDTERDRETR NLADLKQIKIDLGKFSDNPDGY IDILRGLRQSFDLTW\RDIMLLL NQTLAPN
4554	34922	B	4595	1	735	
4555	34923	A	4596	70	624	PTAMVEEGIAAGGVMDVNTAV QEVLKTALIHDGLARGIREAAK ALDKYVYQSQYCGFLQPDQKL ATQGKKGMGVHGVKRKSS*M ASVLPGNLRKRRQAH\LCVLAS NCDEPMYVKLVEALCAEHQIN LIKVDDNKKLGEWVGL\CKIDR EGKPRKVVGCSCVVVKDYGKE SQAKDVIEEYFKCKK
4556	34924	A	4597	145	682	SWRNRTVSNGSAVSASSVHLCF AECKALCGERILTDGSDVSRPTI AAGGVTDVNTALQEV\LKTALI HDGLAR\GISRTWPKAL\DKRQ AH\LCVLASNC\DEPMYV\KL\V EALCAEHQINLI\KV\DDNQET* EKWV\GLCKI\DREG\KPRE*WL VGS*CSSLRTIGKESQAKDVIEE YFKCKK
4557	34925	A	4598	252	590	RSLDLVWWQLSGGLAGSAKPK PCTPVKQSTVMSFPSHKEQYFL MDGKKK/YDKESEKYYSILEKH LNLSAKKKESHLQENSSGPSVS TKLINLFSKRLLCAFLPAQLTPY SFCS

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4558	34926	A	4599	1	1662	
4559	34927	A	4600	4430	4904	LIKGTRCLGRRPSFAYSRSNI*A *S*P/EGTSAQLAELLALTLALE LGNGKRINVYTDSKYAYLILHD HAAIWKERAFLTSGGTPIKYHK EIMELLHTVQKPKEVAVLHCQS HQKESSPLEDTTTAGPLLHPYP AGSSPERSSPSSQQLLGDLFRGII
4560	34928	A	4601	1	2630	MEQANHPVRLINVVCKDTLKKI VQQETSCPLTHVHYAEAITGRC TAPEDKGSLDQKPPTDDPTGCP WQVPAHVITLTETWVCLTIEGQ EIDFLLDTGVQKPNGQWRLVQ DLIPIKEAVIPLYPVVPNPYTLIS QIPEKAEWFMALDLKDAFFCIS LHSDSQFLFAFEDPTNHTSKITR TVLPQGFRDSPPLFGQALAQDL GHFSSPGTLVFQYVDDLILATSS EASCQQATLDLLNFLANQGKV VPNLWGKLPLNTTRKSWSYCT QCKNPRRWQSYTAKAIKKQLA EAGPVTAILLLLIFGPCIFNLLIK FVSSRIEAIMLQMVLQMEPQMS STNNFYQGPLDRCTDPLSGLES SPRCSEAPCLMSQWTGDIEYDL LLPPIPHQTTLCDLQNLKGIFSR YHRKWYGEILALLTPTANVCG HSQVPHACSIYHDPVTWNPQG LLPKSLYGVTKWGDKEHFEWG SQQQRAFYELK\KKLMSAPALG LPDLTKLFTLHVSDREKKMAV RVLTQTMGPWLGPVAYLSKQL DGVSKSWPPCLRALAATALLA REVDKLTLGQNLNIKAPHAVV TLMNTKGHHWLMNARITRYQS LLCDKPHITIEVCNTLNPTTLLL VSESPVEHNCVEVLDSVYSSRP NLRDHPWTSVDWELYVDGSSF INPQGESVWGIIQGKRPIKLWG KRRKVSARDLAIIGGSVEAPKL
4561	34929	A	4602	1	506	FLALTSRFLFVLLNEETRSHLEK SLCWKVSPHIKMDLLQWIQSK AQSDGSTLQQGSLEFFSCLYEIQ EEEFIQQALSHFQVIVVSNIASK MEHMV\SSFCLKRCRSAQVLHL YGATYSADGEDRARCSAGAHT LLVQLPERTVLLDAYSEHLAAA LCTNPNLIELSLYR
4562	34930	A	4603	3	381	
4563	34931	A	4604	3	483	
4564	34932	A	4605	3	410	

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4565	34933	A	4606	2	249	SADAPMFDMGVNHEKYDNSL NII/SVMKAGPVEKRPAWHPMD TLP*LAPRSLFLCSNASCTTNCL EPLAKVIHDNFGIVEGLMV
4566	34934	A	4607	2	481	LAPLVKEIHDNFGMGEGLMTT GHAITATHKTADGPSGKLWRD\ GRGAHQNIIPASTGAAKAVGK VMPELNGKLTGVAFRVPTANV SVVDLTCRRQKPAKYDDIGKV VRQAPEGPLKGILGYTEHQVVS SDFNSDTHSSTFDAGAGIALND HFATLSPPPH
4567	34935	B	4608	79	278	
4568	34936	A	4609	2	1201	PSTACRNSARACSTVSRIFFCVA SRATSLRTPMGKVKVGVNGFG RIGRLVTRAAFNSGKVDIVAIN DPFIDLNYMVYMFQYDSTHGK FHGTVKAENGKLVINGNPITIFQ ER\YPSKINWG\DAGAEYVLEST GAFTTMENAGAHLQGGAKRVI ISAPSA\D\APMFVMGVNHEKY DNSLKIISNA\SCTTNCL\APL\A KVIHDNFG\IV\EGLMTTVH\AIT\ ATQKTV\DGPSGK\LWALMGPR GFFQEHQSLPFTGGC/ARVVGQ GSSPELERGKLTWAWAFRCPQ LPKRVNGWDL\TCRL\EKPCPK YD*HQGRVVKAGRRKGPLQGA ILGLQLSNPGGSPSGLSTSDNPL LPPFDAWGLAFALQRTHFCSKL IFLGIDNGILGYSNQGGWDLHG PPWPTWAFQGS
4569	34937	A	4610	61	226	WRIMPTKKVMITMGRTTQRRM LES/SQQFWPCHLH*KLVPSCLQ LGCLVFHFRRER
4570	34938	A	4611	153	495	QHAAECKAHAGLPGLPLPARK LASRHGAPRWRQSGVGPGGKV ENYGRRRL\PGTRHPQSLSHKP AKKIDVARVTFDLYKLNPQDFI GCLNMKATFYDTYSLSYDLHC CGAKRIMK
4571	34939	A	4612	1	643	
4572	34940	A	4613	286	698	ESDNNLTQGTSI*QGTRHPQSLF PLSPAKKI*CGPVLTFLTCYKLN PQGLSLGCLNIEGRFFMDYVIPF PIDLALLLGAKRIMKG\TLHWA LFSMQTTGPRA/VFTSCYLQQL LDATEDGHPPKGKASSLIPTCL KILQ
4573	34941	A	4614	59	294	
4574	34942	A	4615	1	2253	

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4575	34943	A	4616	2	197	LARSGMGFYRRGLLGEVKGRV EGNRMWHVIVRTSPNHRYTFT LKTHPSVVPGSIAFSLPQ\RPWS
4576	34944	A	4617	302	441	
4577	34945	A	4618	944	1257	RLPFSPRSVGPTPQAPRLLCNG WRQLPTTFFTELEKTTLKFIWN QKRALIAKTI/LKPKNKAGGITL PDFKLYYKATVTKTARFLLYK VSQIDNTDLFDPVKIKFE
4578	34946	A	4619	1	1370	MNIDAKILNKILANRIQQHIKKL IHHDQVGFIPGMQGWFNIRKSM NVIQHINRTKDKNHMIISIDAEK AFDKIQQPFMLNTLNKLGIDGM YLKIIRAIYDKPTANIILNGQKL EAFPSKHGTRQGCPLSPLLFNIV LEVLARAIRQEKEIKGIQLGKEE VKLSLFADDMIIYLENPIVSAQN LLKLIGNFSKVSEYKINVQKSQ AFLYTNNRQTESQIMSELPFTIA SIRIKYLGI*\LTRGVKDLFRENY KPLLNKIKEDTNKWKNIPCSWV GRN\NIMKMAIL\PKVIYRFNAIP IKLPMTFFTELEK\TTLKFIWNQ KRARIAKSILRQKNKAGGITLP DFKLYYKATVTKGAWFQHHK HTLIKEPLLDSVFSPNRPDHGK KQDKQPQTKNIANASADSKNT QQMNGFVTGAATSFIPKDRTAS SLCGCTGRRRQSVAKYLRIRPHI NVPSFTYYK
4579	34947	A	4620	2	671	WHQNLALTRASGSFHS/WEEG KGGADMSHEICVANLQVYVRS TDFDRTLMSAEANLAGLFPPNE VQHFNPNISWQPIPVHTVPITED RLLKFPLGPCPRYEQLQNETRQ TPEYQNRSIQNAQFLNMVANET GLTNVTLETIWNVYDTLSCEAP SPPWGRKPPLERLWPRPRELTC PLRYT\QTHGLLLPPWASPQTV QRLSQLKDFSFLFLFGIHEQVQ KARLQG

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4580	34948	A	4621	1	1923	DSVAFEDVAVNFTQEEWALLG PCQKNLYEDVMQETIRNLDCG HETEFVEYENLRDPMNMPLHT TDGPHKCKICGKGFDCPSSLKS HERTHTGEKLYECKQCGKALS HSSSFRRHMTMHTGDGPHKCK ICGKAFVYPSVFQRHEKTHTAE KPYKCKQCGKAYRISSSLRRHE TTHTGEKPYKCKCGKAFIDFYS FQNHKTTHAGEKPYECKECGK AFSCFQYLSQHRRTHTGEKPYE CNTCKKAFSHFGNLKVHERIHS GEKPYECKECGKAFSWLTCFLR HERIHMREKPYECQQCGKAFT HSRFLQGHERIHTGEKPYECKE CRKAFSWLTCLLQHERIHTREK PYEGKQCGKAFTHSRFLQGHE RTHTAKKLCECLSTVSARKSVD LIIASYPLFLNLFSTPKTLRNCSY RRHERMHTGEKPYECKQCSKA LPDSSSYIRHERTHTGEKPYTCK QCGKAFSVSSSLRRHETTHSAE KPYECKQCGKTFHHLGSFQIHM KRHTGDRPHKCKICGKGFDRPT LVRYHERISTGEKPHECKQCGK AFDHLGSFQRHMIRHTRDGPH KCKICGKGFDCSSTLQSHERTH TGEKKLYECKQCGKALSHSSSF RRHMTMHTGDGPHK\CKICGK
4581	34949	A	4622	1	256	MGKGSFKYAWALYKQKAECE RGVTIDTSLWKFETSKCYVTI\K DFIKNIITGTSQQGQTASVAAFC ILSSCPASWKNQVSHRLGG
4582	34950	A	4623	173	717	SINAVASTRRTIEKFEKEAAEM GKGSFKYAWVLDKLKAERERG ITIDISLWKFETSKYYVTIIDAPG HRDFIKNMITGTSQADCAVLIV AAG\VGEFEA\SICQNG\QTREH ALLAYT\LGVK\QLICRVNKMD STEPPYSQKRYEEIVKEVSTYIK KIGYNPDTRAFVP\ISGLNGDH MLEPKC
4583	34951	A	4624	3	525	GCPSGPGHRCVAGHGAPGAVC RHVPTAWPGYSRCSPGPGPRGV EAVGHQRHRAPETHSTPAADR HRRGLPGS\KSDSAMEPSPSPAP QAQPPKPVPKPRTVFGGLSGPA TTQRPGLSPALGGPGVSRSPEPS PRPPPLPTSSSEQSSALNTVEMM PNSIYFGLDSRGRAQAAQDK

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4584	34952	A	4625	2	448	RRAHACARRRRKKEMLGVNVL TSHSSQERMKLTFKKKAVNFA DAAAAQGPLLPAMVNPTMFFH IAVDGEPLGCVSFEVRGLESKK *LLI*SIKLC*QIG\LFADKVPKT AENFHALSTGEKGFGYKGSCFH RIIPGFTCQSGDFTRPTA
4585	34953	A	4626	1	751	GTRDATAEENRVLLAMVNPTV FFDIAVDGEPLGRVSFEVRGLD TKK*LLI*SIKLC*QIGGSSIFITS D*KNSCLPLIVQQCLLFLRILP\L FADKVPKTAGV*FFFKQKIFRA LSTG\EKGFG\YKGFPAFHRIIPG FMCQGW*LSHRHNGTGWQVH LMGRNFEDE\NFILKAYGVLGS LSMAKCLDPTKIGSPVFPSCTA KT\EWL\DGQALWCFGK\VKKG LNIVEAMERF\GSRNGKTS\KKI TIADCGQLE
4586	34954	A	4627	3	615	PECIIGIDILSSGQNPHIGSLTGR VRAIMVGKAKRKPLELPLPRKI LNQKQYRIAGGIEEISATIKDLK DAGVVIPTTSLFDSPIWPVQKT DGSWRMTVDYRQINQVATPIA AAIPDVASLLKQINTSPDTW/PI RPPISNGD*GVSGR*ACCLEPLA GPHR*ITSEASRILEQGPAIFCR* LLSF*ETALGLLLGFGGN*TFDY
4587	34955	A	4628	3	354	DSWA\VANGLA\GWS\GTWKK HDWKI\NDNEIWGK\SMWIDLS EWSKTVKIFVSHESAHHIT*KSS AEEDFNNQVDRMIHSVDTTRPL SPATPVIAQWTHEQSGHGGRD GGYTWAQQHGL

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4588	34956	A	4629	281	1529	VRVLSPVEKELKLWKNTHKLL SYPTVGAAVTQLQNLTAMGVI GSHGARGQVVALNRQRQGDL QPFTRVTVHWGKG/NMQIFGGL LDTGSELTLIPGDPKHHCGPPV KVGAYGGQVINGVLAQVQITV GPQTHPVVISPVPECIIGIDILSS WQNPHIGSLTGRVRAIMVGKA KWKPLELPLPRKIVNQKQYHIL GGTVEISATIKDLKDTEAVTPTT SPFNSPIWPVQKTDGSWRMTV DYCKLNQVVTPIAAAVPDVVS LLEQINTSPGTWFEWSPK\KAL QQVQAAVQAALPFGPYDPADP MVLEVSVADRDAIWSLWNAAI GESQRRPLGFWSKALLSSADNY SPFERQLLASYWALVETERLTV GHQVTLRPELPIMNWVLSDPSS HKVSGAQQRSIIKLKWYIHDW
4589	34957	A	4630	453	719	ARGSKHTGLIAQWAHEQSGHG GRAGGYAWAQQHGLPLTKAD LP\AMATAECPICQQQRPTLSPR YGTIPW/WAWDAPGGRGCWRL QKAGE
4590	34958	C	4631	122	325	
4591	34959	A	4632	1	346	MAGEKVEKPDTKEKKPEAKKA DAGGKVQEGTGRYSRSAMYSR KAMYKRKYSAAKSKIEKKKEK VLATVTKPVGGDKNGGTQVF\ QIITYSSYTQKVQLPKSTLKQRQ GPCPQGAL
4592	34960	A	4633	115	905	EAFQTLHFCCLGLRQGTKRMA GEKVEKPDTKEKKP\EAKKVDA \GGKVKKGNIKA\KKPKKG\RPH \CSRNPVLCSEGFGRYSRS\AMY SRKAI\YQEGSTFSPLKSKVEKK KKEKVLATVTKPVGGDKNGGT RVVKLRKMPRYYPTEDVPRKL LSHGKK\PFSQ\HVRKLRASITP\ GTIL\IILTGRHRGK\RVVFLK\QL AKLAYLLC*LGPLVLNRVPLRR THQKFCHLPLSTKIDISNVKIPK HLTDAYFKKKKLRKPRHQEGEI
4593	34961	A	4634	2	350	FVALAAVLCRQCLPRAWVCRR AGQGSGRHYRAAICAELKKPLT IEEVAP/DPVGPHEVRVDVHFC GVNFGDILICRDQYQERPHLPFT PGPVADSRKGLPIRSCCPPYNL WHCDFCS

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4594	34962	A	4635	1	556	MGLKLNTHMDQTRGSLSGDTL EGSPSKRAKHLKRGGFRGILGG VGVQERRTGQRPALPCHDLRR AEVVPDHRRGGPRPVGPHEDL WQIPEKVSLQEAAVLPITYGTE SFALEHRARTQPGEIVLVTAAA GATGLAVMWQQISSGQGNIAA AGSDEKCKLAM\EKGAQSSVN YSQGSLKDSATDQ
4595	34963	A	4636	1	142	
4596	34964	A	4637	2	368	
4597	34965	A	4638	2	504	HKVGHAQHHSFITWKWYTRD WSRAGPEGT\GVPYDQLTEEEK TRAWFTDGSARYAGTIRRWTA AALQPLSRTSLKESGEGKSSQW AEVRAVHLVVHFTWKEK*PDV RLYTDSWAVANGLAGWSGTW KKHDWKIDDNEIWGRGMWIDL SEWSKTVKIFVSHESAHHIT
4598	34966	A	4639	182	840	RTAVKGNLPTTPVI/SQWAHEQ SGHGGRDSGYTWAQQHGLLIT KADLAMTTAECLISQQQRPRLS LQYSSIPWGNQPATWWQIDYIR PLPSWKGQSQDSQDRSRNQGV KVKVAPLTITPSDTTAKFLLHV PAALHSAGVDVLVPEGGMLPP GGTTTIPLNWKLRLPPGHFGLLI PLSQQAKKRVTVLAGVIDLDC QDEISLLLYNRDAKELYRYTAH
4599	34967	A	4640	3	283	SRVSCSPPPLSPPPPLSPPPPLSPP PLLSPPPPPLSPPPSPPPPVSLPPP PPVFSFPSSCP/PPFPPPLLPPLPPP PPLSPPPPPPPWSPSPPI
4600	34968	A	4641	1	531	MGSSHCTQPGMLAAAVGQAVP GTDTGADSVSLSASCCHQHAIH CAQAIRAKGHLQAHTELPSAPT QPPSCARQCPKSGGDLGGRELY NNHEIRSGKHIGVCISFANNRLF VVSIPKSKTKEQILEEFIKVTGS YWVLGLSFDFRKWPV/GQCCQ SFHGRLRATPARRAERRDARSF AL

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4601	34969	A	4642	115	2405	ATAEGSGSSGVKERGAGIRKAE RRRTEASGGGGGRGRRRSWRR AGAEGVSEADARGRGGKGREG KGGSRGGARAHRERARRRVEL DRVCCQRRELRPPFYNSSTRAG HREQRARVSRNPIPSDRISPPQP NGEISGNMATEHVNGNGTEEP MDTTSAVIHSENFQTLLDAGLP QKVAEKLDEIYVAGLVAHSDL DERAIEALKEFNEDGALAVLQQ FKDSDLSHVQNKSAFLCGVMK TYRQREKQGTKVADSSKGPDE AKIKALLERTGYTLDVTTGQRK YGGPPPDSVYSGQQPSVGTEIF VGKIPRDLFEDELVPLFEKAGPI WDLRLMMDPLTGLNRGYAFV TFCTKEAAQEAVKLYNNHEIRS GKHIGVCISVANN\RLFVGSIPK SKTKEQILEEFSKVTEGLTDVIL YHQPDDKKKNRGFCFLEYEDH KTAAQ\ARRRFN*VGKVQGFG GNVGTVEWADPIEDPDPEVMA KVK\VLFVRNLANTVTEEILEK AFSQF\GKLERVKKLKDYAFIHF DERDGAVKAMEEMNGKDLEG ENIEIVFAKPPDQKRKERKAQR QAAKNQMYDDYYYYGPPHMP PPTRGRGRGGRGGYGYPPDYY GYEDYYDYYGYDYHNYRGGY EDPYYGYEDFQVGARGRGGRG ARGAAPSRGRGAAPPRGRAGY SQRGGPGSARGVRGARGGAQQ
4602	34970	A	4643	2	369	
4603	34971	A	4644	1	1002	MNAGCGQTHDCAYRQKRPED VNEEGRLEQRNRKRQDEWGPR DKPASSGYKAGTLDVENWNRA GEGLKHAHQKGLKVDSSAFCT CSLIRTVLMPLSPYYSAGQQAE SKNLKESVVPPTASIENKKQER EDKNWPILPPPVAETSVPPPSVA GIETPIQRILRSAAIAGEPSGPCA FPISVRPDSNNPQQFIHEHTPLEF KLLNELKTSVVNIGVQSPFTLG LPESAFGAMRLLPFDVKHWAR TCLSASAYLTWNLNGQEMCTD QVRQNRAAGHGDIAEDMLLGN GP/YFRPGTSNGTKRAWATIPEE GVPVQSFLPFMEGSQEPSAQFL ARLREAV
4604	34972	B	4645	1	575	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
4605	34973	A	4646	1	776	VVLMRNLMSGTIFSMLANISML GSLVIIIQYITQEIPDPSRVPLVA SWKTYPLFFGTAIFSFESIGVDL PLENEMKNARHFPPILTLGMPI VTTLDIGMAALGYLRFGD\DTK GSIILSLPICWYLHGLSGEGPSQ SFSERETKAQVIVPRSEVNVPRR PVSEHSGRGEQLCGLSCRLYQS VKLLYIAGILCTYALQFYVPAEI IIPFAISRVSTRWALPLDLSIRLV MVCLTSAPMTRSTPFCKYSTRG RRRWLEIPV
4606	34974	A	4647	1	1294	MGKDFMSKTPKAMATKTKIDK WDLIKRKSFCTAKETTIIVNRQP TEWEKIFATYSSHKELISRIYTE LKQIYKKKTNNPINKWAKDMN RHFSKEDIYASKKHMKKCSSSL AIREMQIKTTMRYHLTPVRMEII KKSGNNRQPIVGPCDNSVILLY KILANRIQQHIKKLIHHDQVGFI PGMQGWFNTCKSINVIQHINRT KDKNHMIISIDAEKAFDKIQQPF MLKTLNKLGIDGMYLKIIIAIYD RPTANIILNGQKLEAFPLKTGTR QGCPLSPLLFNIVLEVLARAIRQ EKEIKGSQLGKEEVNLSLFADN MIVYLENPIISAQNLPKLINNFS KVSVCKINVQKPQAFLYTNNR QTESQIMSELPFTIASKRIKYLVI QLTRDVKDLFKENYKPLLNE/I K/EDTNKWKNIPCSWVGRINIV KMAILSK
4607	34975	A	4648	2	711	WNRRRPCIAKTIL/SQKNKAGGI TLPDFKVYCKSTVTKTAWYWY QNRHIDRWSRTETSEITPHIYNH QIVDKPHKNKQWGKDLLFSKW CWENWVAICRKLKLNLFLTRY TKINSRWIKDLHEKLKTIKTLEE NLGNTIQDIGIGKDFMTKMPKA IATKAKIDKWDLIKLKSFCTAK ETIIRVNKQPTEWENISAIYPSD RSLISRIYKE\LKNIYKRLDAVA HTCNPITLKGQGRWIT
4608	34976	A	4649	1	576	
4609	34977	A	4650	1	771	

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4610	34978	A	4651	1	887	FPEDSEPISISHGNYTKQYPVFV GHKPGRNTTQRHRLDIQMIMIM NGTLYIAARDHIYTVDIDTSHTE EIYCSKKTAWEILDRPMVATCR MKGKHKDE\CHNFIKVLLKKN DDALFVCGTNAFNPSCRNYKM DTLEPFGDEFSGMARCPYDAK HANVALFADGKLYSATVTDFL AIDAVIYRSLGESPTLRTVKHDS KWLKEPYFVQAVDYGDYIYFF FREIAVEYNTMGKLLGLHHELL RRTQDYGHKAGCPESCLLSVRR CPPPQSKAHRESVEELIKGCRR HAGFCACGHITT
4611	34979	A	4652	1	2890	MVLLKVDPGLWGSSLRVLLKA DPPYGTQAHAERHGRALAGGL GVGEQSQSLDLLRMSHTYGAL FLPRAAVSSWCASVRIRKIKKSP LLDGAPLLYEPDTWLGKWSSS WTLVFTHPFSAALTHSALTARS DTGSLTLSPDGKLYSATVTDFL AIDAVIYRSLGESPTLRTVKHDS KWLKEPYFVQAVDYGDYIYFF FREIAVEYNTMGKVVFPRVAQ VCKNDMGGSQRVLEKQWTSFL KARLNCSVPGDSHFYFNI
4612	34980	A	4653	1	480	MEGVEEKEKVPAVPETLKKKQ GNFAELKIK\PKMAFVLRIRGVS GVSPKVRKVLQLLRLHQIFSGT FVKLN/KASVNMLRIVEPYIAW GYPNLKSVNELIYKRGYGKINK KRIALTDNTLIVPSLGKYGILCM EDLIHEIYTVGKHFKEANNLLW PFKLSSP
4613	34981	A	4654	3	279	
4614	34982	B	4655	119	177	
4615	34983	A	4656	157	359	HQRCRK**TKLEG*TCRKIEVN TDYIKP*E*EFWMIYYISIYLTSI CSSICNENILQLENREKSRNT

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4616	34984	A	4657	65	900	GLAFPPILQKESPHPCLWILFTSP VALSTSRPPCVISSAALCPRRHG FLPPRLLAPLAAAFCPRPRCFLP LPPRLFAPAPVDFCPRRCGFLPL PPRVFAVSCPRRRGLLPPLLFAP SAAAFCGFLAPSPWLFAAFGTR CRGFLGLLVPAAAAFFPRRLRF FLPRLFSPAAAVTFCHPCFLPPP PRLSVPAAASFCRRGFQQEIRTV EIRGSGTRVGLQHQTGHLPRGP SSLPAELHA*ARVSPLEASPPSC TR/WMQQPEDLGPALTLGRICG VGACWEL
4617	34985	A	4658	927	1157	ARRSTAPVDCK*LQP*AQAAL WVLVWDHEAARQPEGVVQPA PGLWPSSRRWRKFQAPGSSGV CHPGALQACPEELS
4618	34986	A	4659	1	563	MKLVAVFDKQDLHHGGDDISA SSMHTQSPERFTSASELGTNNV SAFSV\YQAASEIEVTSSVLHAS SQKGLSSQHLGFGAPQAGGGSF RHLAPQRKEVLEEYFKYDPEH KLIFRFVRTLFKAMRLTAEFAIE ITHGGRDVERATGLVNKIHRQG CGDSFCNIGGNAKPYVCCGKE YVSSSKHQNGIAI
4619	34987	A	4660	1	681	MGKYAEALRSQQKAVLMSVR VMGIEHPNTIQENMHLALHCFT SRQLSLALSLLQGAHYLM/LLV LGE/DHPEVA/LLDNIRRVLHRV MEYDLSLCFLDNALAVSTKYQ GPKALKVALGHHLITSVYESKA EF\RSALQHQKEGLAAH/TSLGE DQEKTKESSEYLKCLTQLAVAL RRAMHEIYRNGSSNNIPPLNFT APSMASVLEQFKGINGILFIPLS QKDLESLKAEVAQ
4620	34988	A	4661	2	443	VWQSGGDSITSKTNIITCVNCY LYTCIDSSFNQYHSILIVRARQD IWLPVALHRPWESSPFIHVINNI LQKILKRSTQFIFTLIAIIMGLIA VTVIAATAGVALRQSIQTVHFV DKWQKNSTRMWNS/QRIDQKL ANQINDLRQTVIW
4621	34989	A	4662	2	377	FAFTWTDPDTHQAQQITWALL PQGFADSPHYFSQAQISSSSITY LGIILHENTRALPADHV*LISQT PISSTKQQLLSFLGMVRYFCLWI PSFTILTKPLY*FTKANLADPTD PKSFPHSSFRSL

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4622	34990	A	4663	1	1095	MAKAVLSKKNKTGSTTLPDFKI YYKDIVTEEPGIETLRHTSSTKF SKGLPSRESFSEKQNKTTTHLH PGEINSFIAHTKPAWRSLHTDA HEIWCRDSDQVNSPGRSIPCPPA LCSMRKIHLRPLVLRPASPRNIS PILNPLHLIAALLPNPKPPFRPPL VSPDLNPQVKDISTPSWATDHV HLTVSLKPYHPYPAQCQYPIPQ HALKGLKPVITRLLQHGLLKPI NSPYNSHILPVLKPDKPYRLVV QDLRLINHIVLLPIHPMVPNPYT LLSSIPASTTHYSVLDLKHAFFT IPLHPSSQPLFAFTWTDPDTHQA QQIT*AVQPQSFTDSPHYLNQA QISSSSVTYLGIILIKAHVLSLPIV
4623	34991	A	4664	655	2417	KKRESMNIDAKILNKILANRIQ QHIKKLIHHDQVGFIPGRQGWF NICKSINVIQHINRAKDKNHMII SIDAEKAFDKIQQLFMLKTLNK LGIDGTYFKIIRAIYDKPTANIIL NGKKLEAFPLKTGTRQGCPLSP LLFNIVLEVLARAIRQEKEIKGI QLGKEEVKLSLFADDMIVYLEN PIVSAQNLLKLISNFSKVSGYKI NVQKSQAFLYTNNRQTESQIMS ELPFTIASKRIKYLGIQLTRDVK DLFKENYKPLLKEIKEDANKW KNIPCSWVGRINIVKMAILPKVI YRFNAIPIKLPMTFFTELEKTTL KFIWNQKRAHITKAILSQKNKA RGITLPDFKLYYKATVTKTAW YWYQNRDIDQWNRTQPSEITP HIYNYLIFDKPDKNKQWGKGS LFNKWCWENWLAICRKLKLDP FLTPYTKINSRWIKDLNVRPKT TKTLEENLGITIQDIGMGMDFM SKTPKAMATKDKIDKWDLIKL KSFCTAKETTIRVNRQPTKWEK \FSQPTHLTKG*YPESTMNSNKF TRKKQTTPSKSGRR\NEQTLLK RGHLCSQKTHEKMLTITGHQR NANQNHNEIPSHTC

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4624	34992	A	4665	1	234	MQNQEKFGELISEWAPYGRPRP QIAVGDHHISVYDGEVNWRMS SLQASAAGKDYANRGTEWGEE PSQMLRHELLSGEMCVSRNRG QPLANSERRSEALSPVTPKKLIP ADGHKSDPGRTWMKLETIILSK LTQEQKTKHHMFSLISG*FAEN DGFQLHPCPS\GSLLWPSAGISF FGVTGLRASDLLSLLARGCPRF LDTHISPLSSS
4625	34993	B	4666	1	2553	
4626	34994	A	4667	33	272	
4627	34995	A	4668	1	3045	
4628	34996	A	4669	1	334	
4629	34997	A	4670	159	245	FPIVASPWLLC*LMSFAGTWVK LETIILSKLSHGQKTKHRMFSLI DTVVVGSDDFPLLRVPGCCASS LNAAHTSVNIKLELT
4630	34998	A	4671	122	359	TANLKNGRKFL*PIHLTKG*YPE STKNVNKFTRKKQTTPSKSGQK I*TNTSQKKTFMQPTGT*KNAH HHWSSEKCKSKP
4631	34999	A	4672	2	66	RLVYADTCFSTIKLKAEDASTS ENMRCLVFCACDSLLRMIVSSF IRVPTKDMYSSFFMAA*YLLQY HQVKSRRCFYE
4632	35000	A	4673	519	899	SALVCHTCSNWQVHLGDSVFY RSEEQPLEPLPFSYLSSLFPGLHP DPVSSGSQQPS*MPHTDASVTS SHGLGGLAGRNSCIYPCCAPAL CADYLWGSPDLFLLLSFQHKG NVGVGLAHSPQFQQGN
4633	35001	A	4674	1	278	
4634	35002	A	4675	158	592	GYYWRPSFQSLRENNECQRKS NSVNAGCLNCDHCVLGIYQQH *QNYFSFDIHYFLSETGRKVSSS I/AYFTIGETEALSGKVVPYWQQ AAGQGCTLHLLLPQTRLFPGKG RRQPGLLREF
4635	35003	A	4676	302	721	
4636	35004	B	4677	1	871	
4637	35005	B	4678	1	559	

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4638	35006	A	4679	3	2386	RVATMAPHRPAPALLCALSLAL CALSLPVRAATASRGASQAGAP QGRVPEARPNSMVVEHPEFLK AGKEPGLQIWRVEKFDLVPVPT NLYGDFFTGDAYVILKTVQLRN GNLQYDLHYWLGNECSQDESG AAAIFTVQLDDYLNGRAVQHR EVQGFELAP\FLGYFKSG\LK\Y KKGGVASGFKHVV\PNEVVVQ RLFQ\VKGRRVVRATEVPVSWE SFNNG\DCFIL\DLGN\NI\HQWC GS\NSNRYERLKATQVS\KGIRY NERSGRA\RVHVSEEGTEPEA\M LQVLGPR\VALPAGTEDTAKED AAN\RKLAKLYKVSNGAGTM\ YVSLWAD\ENEFTQGA\LKSED CFILDHGKDGKIFVWK\GKHAN TEERKAALKTASGFHSPRWDY PKQIQVSVPFLEGG\ETPLFKQV FKNWRDPDQTDGLGLSYLSSHI ANVERVPFDAATLHTSTAMAA QHGMDDDGTGQKQIWRIEGSN KVPVDPATYGQFYGGDSYIILY NYRHGGRQGQIIYNWQGAQST QDEVAASAILTAQLDEELGGTP VQSRVVQGKEPAHLMSLFGGK PMIIYKGGTSREGGQTAPASTR LFQVRANSAGATRAVEVLPKA GALNSNDAFVLKTPSAAYLWV GTGASEAEKTGAQELLRVLRA QPVQVAEGSEPDGFWEALGGK AAYRTSPRLKDKKMDAHPPRL
4639	35007	A	4680	1894	2161	MFGLPNARAATSTAPFASHSLC LCFRILLLLGPGINLANPRNHLV LHQKFSILGRHFSL\ATEEPCISL ALAPSKRWECNSSS*RYENN
4640	35008	A	4681	1	1803	
4641	35009	A	4682	1	501	MTFQCVVNTHYLTYPRPQRFL YLVVVRPSCASWIMFVLIDRGY VFSYFPQSYGGFGSRILSKPIEV QVGGRSVVAQMWSNKCGQYS DLASLGCISR/YSAGSVYYYPSY HHQH/NPVQVQKLQKELQRYL TR/KIGFEAVMRIRCTKAKPTRH RHYGELEISITIIRAIGK
4642	35010	A	4683	350	623	

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4643	35011	A	4684	1	3252	PPGPERSRLGLGVSLHQRSCPK CIAVFTRVSEPRIQFPASRILPSS NTSKDFDPVSGQSNYGGSQGS GQTLNRPPVASNPVTPSLHSGP APRMPLPASQNPATTPMPSSSF LPEANLPPPLNWQYNYPSTASQ TNHCPRASSQPTVSGNTSLTTN HQYVSSGYPSLQNSFIKSGPSVP PLVNPPLPTTFQPGAPHGPPPAG GPPPVRALTPLTSSYRDVPQPLF NSAVNQEGITSNTNNGSMVVH SSYDEIEGGG
4644	35012	B	4685	51	236	
4645	35013	A	4686	1004	1405	
4646	35014	A	4687	1	771	
4647	35015	A	4688	1	405	SENVDDVSVMMG/TPANKALL DTTGFWHD/DFNNATPNDICVA IRSE/AADAGIAQAIMQQLEEA/ LKQQA/LDRNLNVMMFSDNVT LE/DEIQLK/TRAREKGLLV/MG PDCGTSMIAGTPLAFA/NVMPE GNIGVIGASGTGFRR
4648	35016	B	4689	1	1656	
4649	35017	A	4690	1657	2259	LPQPQPATPWPSAPTPRFASPAA AMATLWSGTCRIRLWSGSSRA TRTAPAALIFPITALGSGQGAW TTRCAAGTCGRAASCSSMTSA/ AQIFSPCHCPNQDWLAVGMESS NVEILHVGKPEKYQLHLHESCV LSLKFAPCGRWFVSTGKDNLL NAWRTPYGASIFQSKESSSVLS CDISRNNKYIVTGSGDKKATVY EVVY

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4650	35018	A	4691	62	1371	QNQSTISVMLRSAMTTTMAAD LITAI/MGQRKQHIDTGFWHDD FNNATPNDICVAIRSEAADAGI AQAIMQQLEEALKQLAQGSGS SQALTQVRRWDSACQKLPDAN LALISVAGEYAAELANQALDR NLNVMMFSDNVTLEDEIQLKT RAREKGLLVMGPDCGTSMIAG TPLAFANVMPEGNIGVIGASGT GIQELCSQIALAGEGITHAIGLG GRDLSREVGGISALTALEMLSA DEKSEVLAFVSKPPAEAVRLKI VNAMKATGKPTVALFLGYTPA VARDEN/VWFGSSLDEA\SLAG CFSVRARSPLTRIDGMMILGMF GGCFAASLWANNVKLRMPRSR IRIMQAIIGGIIAGFGARLAMGC NLAAFFTGIPQFSLHAWFFANP LLIGQTLEDPHEYIDYLDKEFPL YQLVECVVSLNYSYHWECTEI
4651	35019	A	4692	1	1125	MEAEVDKLELMFQKAESDLDY IQYRLEYEIKTNHPDSASEKNPV TLLKELSVIKSQYQTLYARFKP VAVEQKETKSRICAGMTKTMN VIQKLQKQTDLDLSPLTKEEKT AAEQFKSHSFGMWPCKLKYRQ NKKKKKKLSQNRSTTWKLNNL LLNDYWIQNEMKAEIKMFFET NENKDTTYQNLWDTFKAVCRG KFIALNAHKRKQERSKIDTLAL QLKELEEQEQTHSKASRRQEIT KIRAELKEIETQKNLQKINESRS CFFEKINKMDRLLARLIKKKRE KNQIDAIKNDKGGITNDPTEIQT TIREYYKHLYANKLENLEEMD KFLDTYNLPRLNQEEVESLNRPI TGSEIEARINSLPT\KKSPGPDGF
4652	35020	A	4693	2	421	GRVGGRVGKIRT*LN*IETKKY KR*NETKSWFFEKIKMDRPLAR LTKKRIKEIQITSLRNETGNIITD TTEIHKIIQG*SSSSSSSSSSSSSSS SS\FSSSSSSSSSSSSSDTFKRPIT GIKIEMVF*KLPTKKSRISL

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4653	35021	A	4694	1	654	MEYYAAIKNNTFMSFAATWM KLEAIILSKLTKEQKTKRHMFSL VSTLELGALTALVRCGRWRRQ CDDEAMACVTQGRPLARLTKK RREKIQITSLRNETGDITTDTTEI QKIIQGYDEHTYAHKVENLEG MDKLLEKYNPPRLNQEELGTL NRPITSYEMEMIIKKL/PNEKSP GPDGFTAEFYQTFKEELVPILLA LFHKTEKEGILPNSFYEASITL
4654	35022	A	4695	1	786	MPPSLAYKNPRPQQADTQVA/T MSRGVHWRKKMQAAGPREDV KRSTQAEEHTDRHQHTSR\HQL LLMRIFEMGWKKPSPFQEESIPI ALSGRDILARAKNGTGKSSAHD IPLLKRLDLKKDTIQTIVIVPTG GPALQVSQICIQVSKHMGGVK VVMTTGGTNSGDDVLRLDDTV HMVIAAPGRILNLIKKGVAKLE ETYLRHIGRPGHFGHFGLAINLI TYGDHFNLKGIEEQLGKEIKPIP SNIDKSLHVAEFHSKAVENEKP
4655	35023	B	4696	1	501	
4656	35024	A	4697	2	573	YSACFFLFSIAMGILLTVPPSFWI PTSFSAFLGFFSSFSLLVLHQPD FSFVLGLWRIISLLVLKIVEGSS NQGMQMASRSWEWPSSSRKM ATSVRTLPEP/GPSGCRAPSAFPF RKEAGADPSGCPGGRQVPLVAI GRGGALEPQRWELRAPGSAGR LPREGGRTFPGAQSPAGAQSPA GKQSPPGAQSPLH
4657	35025	A	4698	2	346	PPINISVPHC*PFGG/EPLEILIPAP ERSSHVLSQSPVRTHSSAVHQS VGASLNCGDKQPPNFSGSKIFF LIYLHLMTGQVRGSSVLCHPNT GIQKEGGTVNEIPIAIEKRKKHA
4658	35026	B	4699	1	468	
4659	35027	A	4700	2	284	ETGEFTQLKELNIQGNCWTLLL PELGNLYLTGQKKVCKVENSP WVTPIAGQFQLDVSCVSECVCS ETYEYLYGQHMQ\ANP\EPPKH NNHKSGKD
4660	35028	A	4701	5	189	
4661	35029	A	4702	38	190	

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4662	35030	A	4703	2	882	WPSVSSG/PSSAVSFSSFDPGVA SCTSSSASGIQRPMASEVPCASG IPIKKIGHRGVDSSGETTYRKTT SSALKCAIQLCITHTVGSLDPTP ERHVLIEPLIELSSSGADGSLLH VSIHDEFIIKTVQHKQAEFLQKL IPGYHIDLNQNSWTLLPKFYGL CCVKAGGKNTQIAVMKNLLLR LNSEGERILLCIGITDILQSYRFV KKLEHSWKALVCDGDTVSVHR PGFYTERFQCFMCNTAFKKIPA RTLTTPNAGKDVEQQELSSLLM GMRSGTATVEDSLVVSYKTKH
4663	35031	A	4704	2	410	
4664	35032	A	4705	2	728	
4665	35033	A	4706	1	1208	MKMEKVNTSWLLPPSSISVLIR RGAGSMVLLLQSQRQYIFEYDS SDRLLAVTMPSVARHSMSTHTS IGYIRNIYNPPESNASVIFDYSD DGRILKTSFLGTGRQVFYKYGK LSKLSEIVYDSTAVTFGYDETT GVLKMVNLQSGGFSCTIRYRKI GPLVDKQIYRFSEEGMVNARFD YTYHDNSFRIASIKPVISETPLPV DLYRYDEISGKVEHF\IITTAEM TLSKHFDTHGRIKEVLA/YEMF RSLMYWMTVQYDSMGRVIKR ELKLGPYANTTKYTYDYDGDG QLQSVACNDRPTWRYSYELNG NLHLLNPGNSVRLMPLRYDLR DRITRLGDVQY/KIDDDGYLCQ RGSDIFEYNFNGAPTKTLSQAS GILQSLQGLHEVHRNPACSDFA
4666	35034	A	4707	1	663	MMLLLLALLGAGLLGASLLTS WHAPARNKIPRAQKWREEPDL DPKPILELPLAELAQQLRTEELS LESILCSYLKQALKVHQEVNCL MDFLGECEEELQALKKLKKSE RGLLYGVPMSLKDTYDSMFLE KPATKDGVIMKVLKAQGAIPFV KTNIPLTLLRSLKRASWALNAA TPIYGQMLSPLNLKKTCGGSS/G GDHGGWPHGPGRGEPGAVPCK

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4667	35035	A	4708	2	624	SDARLHKDDTDICFSKTLNSCK VPQIRYASVERLLERLTDLRFLS IDFLNTFLHTYRIFTTAAVVLGK LSDIYKRPFTSIPV\RRARKLSLT SPLNSKIGALDLTTSSSPTTTTQ SPAASPPPHTGQIPLDLSRGLSS PEQSPGTQPEVSGSSPHSTAQSK IWSLVWKQYWLMAPSHALKT CHAARLARTFVTSSSATKVHCA ISLK
4668	35036	A	4709	1	195	
4669	35037	A	4710	1	1845	MAEAEPGRPGERGGGGAGRAG GRPGGGGGMAEPSGAETRPPIR VTVKTPKDKEEIVICDRASVKE FKEEISRRFKAQQDQLVLILSGK ILKDGDTLNQHGIKDGLTVHLV IKTPQKAQDPAAATASSPSTPDP ASAPSTTPASPTTPTQPSTSDSA SSDAGSGSRRSSGGGPSPGTGE GSPSATASILSGFGGILGLGSLG LGSANFMELQQQMQRQLMSNP EMLLQIMENPLVQDMMSNPDL MRHMIIAKPQMQQLMERNPEIS HMLNNPELMRQTMELARNPAV MQEMMRNQDRALSNLESIPGG YNALRRMYTDIQEPMFSAARE QFGNNPFSSLAGNSDSSSSQPLR TENREPLRNP/WSPSPPTSQAPG SGGEGTGGSGTSQP\GSGMFNS PEMQALLQQISENPQLMQNVIS APYMRSMMQTLAQNPDFAAQ MMVNVPLFAGNPQLQEQLRLQ LPVFLQQMQNPESLSILTNPRA MQALLQIQQGLQTLQTEAPGL VPSLVSFGMSRTPAPSAGSNAG STPEAPTSSPATPATSSPTGASST QQQLMQQMIQLLAGSGNSQVQ TSEVRFQQQLEQLNSMGFINRE ANLQALIATGGDINAAIERLLGS
4670	35038	C	4711	59	464	

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4671	35039	A	4712	1	1902	MAEAEPGRPGERGGGGAGRAG GRPGGGGGMAEPSGAETRPPIR VTVKTPKDKEEIVICDRASVKE FKEEISRRFKAQQDQLVLILSGK ILKDGDTLNQHGIKDGLTVHLV IKTPQKAQDPAAATASSPSTPDP ASAPSTTPASPTTPTQPSTSDSA SSDAGSGSRRSSGGGPSPGTGE GSPSATASILSGFGGILGLGSLG LGSANFMELQQQMQRQLMSNP EMLLQIMENPLVQDMMSNPDL MRHMIIAKPQMQQLMERNPEIS HMLNNPELMRQTMELARNPAV MQEMMRNQDRALSNLESIPGG YNALRRMYTDIQEPMFSAARE QFGNNPFSSLAGNSDSSSSQPLR TENREPLPNPWSPSPPTSQAPGS GGEGTGGSGTSQVHPTVLNPFG INAASLRSGMFNSPEMQALLQQ ISENPQLMQNVISAPYMRSMM QTLAQNPDFAAQMMVNVPLFA G\NPQLQEQLRLQLPVFLQQMQ NPESLSILTNPRAMQALLQIQQ GLQTLQTEAPGLVPSLVSFGMS RTPAPSAGSNAGVYPPRPPLPHP ATPSHIFSNRG/SPAPQQQLMQQ MI\QLLAGSGNSQVQTPEVRFQ Q\QLEQLNSMGFINREANLQALI ATGGDINAAIERLLGSQLS
4672	35040	B	4713	309	527	

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4673	35041	A	4714	1111	2506	KKDQRETRNQKGLGFLRDRPQ WVSGKMKQECLQ/HWNAMAI NNHRAVAIFPKRRHGREDGLLS NLPTFGSYAPLRRVSNEFIASAV QRILLERRALPHGNCKLGGLTP QFMNRKNALVLEVLARAIRQE KEIKGIQLGKEEVKLSLFADDM IVYLENPIVSAQNLLKLISNFSK VSGYKINVQKSQAFLYTNNRQ TESQIMSELPFTIASKRIKYLGIQ LTRDVKDLFKENYKPLLNEIKE DTNKWKNIPCSWVGRINIVKM AILPKVIYRFNAIPIKLPMTFFTE LEKTTLKFIWNQKRARIAKSILS QKNKAGGITLPDFKLHYKATV TKTAWYWFQNTDIDQWNRTEP SEIMPHIYNYLIFDNPEKNKQW GTDFLFNKWCWENWLAICRKL KLDPFLTPYTKIKSRWIKDINVR PKTIKALEENLGNTIQDIGMGK DFMSETPKAMTTKVKIDKWDL IKLKSF
4674	35042	A	4715	3	372	SVGVALRPWKRE/RAASERRSS SGGGGGGGGGGGGGGGSGS GQ/HAPAAPAGGIEAVNMASAS YHISNLLGVLAAAALAVTQALP \PPSAVAGSFSAPKSPAHRSAGL PIPAEPLSSPLLQPPPP
4675	35043	A	4716	1	1008	
4676	35044	A	4717	1	2619	
4677	35045	A	4718	449	801	VLLLSSMSRRKCQSLYVDLLM KKETE*SMEKEKLTMHPLSCTH I*PRPQAPEADKQMRR*TEEQN CRMMWQKKEKEHLNAKRSLA GSGWRDQPLDGKAPGEDHLPIP SPFQLPIHPI
4678	35046	A	4719	1	1255	
4679	35047	A	4720	2	843	CLHGFGYRIRDSELQKIHRAAV KGDAAGVERCLARRSGDLDAL NK/TAQIAGAQPREEACTVILLE HGTNPNLKDIYRNTALHYAVY SESTSLAEKLHFHGANIEALDK VLSISFLSKILMSSLKTCGRDAE DYTISHHLTKIQQQILERKKKIL KKEKRGKASESEFLNSLGGPTL DKKIRNVEISDESAVSILHELCV DSLPALDDEVLSVATKCVPEKV SEPLCRPSHEKGNRIVNGKGEG SEECLCPAAHRLRCGERLYLPP RLGCERLCLATTPSEK
4680	35048	A	4721	295	1050	

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4681	35049	B	4722	306	554	
4682	35050	A	4723	2	7973	
4683	35051	A	4724	2	316	
4684	35052	A	4725	81	228	DPPLCLGLL\LHRASIVQKRIIYF QDEGSLTKKLCEQGKTLKHSQ QMFFK
4685	35053	A	4726	1	1043	MELEWKVNVKVNSQDTNHHG SLQLARGEAAAVKFGRMSKKQ RDSLYAEVQKHQQRLQEQRQQ QSGEAEALARVYSSSISNGLSN LNNETSGTYANGHVIDLPKSEG YYNVDSGQPSPDQSGLDMT\GI KQIKQEPIYDLTSVPNLFTY\SSF NN\GQLAPGIT\MTEIEIVAAEKF PLIYKQSFLLTVLSFGGGGSVIC GPTFAKVSSSRRFIHHGDKIQPS INALGWTFMEETPQIFKCRTNT HGKELEHDLPEHSSGQGSTRRK SSCLRRDNNPMLLSGGRFYEKI HNFITGTFDVRKMEHAEGKTSD LVHVGFQAIKMPSSLKQEASNG LIKLEEASGARMKTGHIK
4686	35054	A	4727	467	584	
4687	35055	A	4728	1	1794	
4688	35056	A	4729	110	1797	PSQQEPGSGTSCLRYCWTAQTL PSVTMKLWVSALLMAWFGVLS CVQAEFFTSIGHMTDLIYAEKE LVQSLKEYILVEEAKLSKIKSW ANKMEALTSKSAADAEGYLAH PVNAYKLVKRLNTDWPALEDL VLQDSAAGFIANLSVQRQFFPT DEDEIGAAKALMRLQDTYRLD PGTISRGELPGTKYQAMLSVDD CFGMGRSAYNEGDYYHTVLW MEQVLKQLDAGEEATTTKSQV LDYLSYAVFQLGDLHRALELTR R\LLSLDPSHERAGGN/LCRYFE QLLEEEREKT\LTNQTEA\ELTTP EGIYERPVDYLPERDVYESLCR GEGVKLTPRRQKRLFCRYHHG NRAPQLLIAPFKEEDEWDSPHI VRYYDVMSDEEIERIKEIAKPK LARATVRDPKTGVLTVASYRV SKSSWLEEDDDPVVARVNRRM QHITGLTVKTAELLQVANYGV GGQYEPHFDFSRNDERDTFKHL GTGNRVATFLNYMSDVEAGGA TVFPDLGAAIWPKKGTAVFWY NLLRSGEGDYRTRHAACPVLV GCKWVSNKWFHERGQEFLRPC
4689	35057	B	4730	1	2433	

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4690	35058	A	4731	425	1079	PMGTSFLYECANFQSVSLGDPQ EPSCLCGGQPQGAAGGSSGSED ALLCLWDLQARKWKFEMSYTS GNIRGSSFCQFKSSFLVYFKALL KFRELFAQFKSFMGEKKLSLAP PMSDSSGDGIIRKIDYASCKRSG \SSIRALPKTYQQP/EVLNDTWV SFPSWSEDSTFVSSKKTPYEEQL HRCEDERFEEMKTAGFASFGER SKTGVPNLRVTDWYRLVAC
4691	35059	A	4732	3	425	GASSEEAEGASEGP\GAPGGWG APGSQGAQEGGDLQEAEESQE GGDPRKPRSPRKVERHRKAGA PGRDLGRPSLTVLL\NHCVLQR LRKIYHSSIKPLEQSYKYNELRQ HEITGQRCPCCEEPKPQHQERA LFVVVSENRNI
4692	35060	B	4733	1	1056	
4693	35061	A	4734	171	511	LLSVRHVVRNTQETANDVQVW /LDREGGSKI\NTGVCFLDHMLD QIATAVSRME\INVKGDLYIDD HHTV\EDTGL\ALGEALKIAPGD KPGICRFGFVLP\MDECL\ACAL DISGGPH
4694	35062	A	4735	563	763	
4695	35063	A	4736	365	1644	RTSQMSSSAWRQQNRARPSSAI LPSSLSLGHPALPQFSQRMPAT ASQLPGMVGVLEGYGQTAASP GSVSSCSPACSSCCLGCWWPSS WPSCRLHPHLGRPIAHCLPE/VL TTTTTTPTITTSQAAGTPKGQQE SGVSPSPQSTCGGLLSGPRGFFS SPNYPDPYPPNTHCVWHIQVAT DHAIQLKIEALSIESVASCLFDR LELSPEPEGPLLRVCGRVPPPTL NTNASHLLVVFVSDSSVEGFGF HAWYQAMAPGRGSCAHDEFR CDQLICLLPDSVCDGFANCADG SDETNCSAKFSGCGGNLTGLQG TFSTPSYLQQYPHQLLCTWHIS VPAGHSIELQFHNFSLEAQDEC KFDYVEVYETSSSGAFSLLGRF CGAEPPPHLVSSHHELAVLFRT DHGISSGGFSATYLAFNATERL CLVESTSS
4696	35064	A	4737	1	154	

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4697	35065	A	4738	1	700	GSRPQFPGHTRVRASGWRPCSL KPQLLGPVHPVSPYLLFLSSSDC AMGLIDGEWQLVLNVWGKVE ADIPGHGQEVLIRLFKGHPETLE KFDKFKHLKSEDEMKASEDLK KHGATVLTA\LGGILKKKGHHE AEI\KPRGTVSNATKHKIPVKVT WRSSPECII\QVLQSKHPGDF\GA \DAQGAMKQGPGSCFRKDNWP PTYKELGLSRAKPLAGFPTPNPS WAPGFKRERGLISV
4698	35066	A	4739	1	154	
4699	35067	A	4740	1	617	GSRPQFPGHTRVRASGWRPCSL KPQLLGPVHPVSPYLLFLSSSDC AMGLIDGEWQLVLNVWGKVE ADIPGHGQEVLIRLFKGHPETLE KFDKFKHLKSEDEMKASEDLK KHGATVLTA\LGGILKKKGHHE AEI\KPRGTVSNATKHKIPVKVT WRSSPECI\IQVLQSKHPGDF\GA \DAQGAM\\NKALE\LFRKD\MAS NYKELGFQG
4700	35068	C	4741	46	522	
4701	35069	A	4742	78	617	TKELLHSKRNCHQSEQATYKM GENFCNLLI*QSANIQNLQRT*T NLQEKNKQPHQKVGEGYEQTL LNRRSLCSQKTHEKILIITGHQR NANQNHNEIPSHTS*NGNH*KV RKQQVSYKLL*MRPRRTRQVT Q*RREPETSLAKETPGNPTNTN AKFKTRGARISHYSSGNGERLP RTVC
4702	35070	B	4743	1	6477	
4703	35071	A	4744	1	623	MSSDISEVEDKNEFLTEQLSKP QIKFNTLKDKFLKTRDTL\RKKS LALETVHNNLSQTQQQIKEMK EMYENAEAKENNSTGKWSCVE ERICQLQHENPCIEQQLDDVHQ KECLPSRKEKFKSEPPAFLSGN QVKSSSCSLQTLFPPDDLILYLE NPKDSTKKLLELINKFRVTGYK IKLQKSVAFLNDKNEQSKEENQ ECNPIYNNYK
4704	35072	A	4745	2	3272	
4705	35073	A	4746	1	579	
4706	35074	A	4747	3	510	

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4707	35075	A	4748	1	1261	MEAVDTFLVFNALNFLLTSQTT GCSSSCDPGHGLGQGSGNRFPI AAASARTAEEAKWFFSNKDYS NVLQLPDPKKTEYHIHEKRFSD SRILCYYPEFGKVEEIILTAMKH DWFGKHRKDDKIEKTGKIKIQE SFTSEEERIRMKQEQERIQAKTR EFRE\RQARERDYAEIQDFHRTF GCDDELMYGGVSSYEGSMALN ARPQSPREGHMMDA\LYAQVK KPRNSKPSPVDSKGKVLGEADP VYPRRNPGTEGNASSLPSVSFSE SPPVRAAFAGYHYVAFPWLQK LMSGTSGKDPEKEADLARVVT LRVVTLRIETHVKTLAFTAALL QQLACIDVGMDKQNDVYTYN KILLSFKRKEILTHTTTRMSLED IILSEINQWQEDKYRFGLYEVA QVVKLIETESKVVVSRDGGRG
4708	35076	A	4749	10	2051	
4709	35077	A	4750	2	2118	
4710	35078	A	4751	1	658	MWNSKTLAAFRPCPKDPLNFE LERDNLAYLAEEIPKQQSIQYIT WMILKAFSHMHLQRDNLKLEL MFKRKAKHKGLKNLHPDHVIE KKNLFSAEKFKPAAEIYISNEEP NVNSQDNGKKCLQGMSEIFAA APAITDNTSDKTTLIKVSSWPYI ADRRCPLVNVTREDSPSEDPVF LRTLGKGDWFGEKALQGWGL\ KGIHHVSAQEPVCLLLPFMTPR
4711	35079	B	4752	1	471	
4712	35080	A	4753	315	407	
4713	35081	A	4754	411	1042	
4714	35082	A	4755	1	423	
4715	35083	C	4756	202	321	
4716	35084	A	4757	5	413	CFFFFFFETESHFVTQAGVQWR DLGSLQSPPPGFTPFS/SPQPPKE PGPQAPATTPGQSFAFLVEMGF HHVSQ\EVSIS*PRDPPASASQS AGTTGVSHRAWTFCFLRQSLA LSPDWSAVARSQLTATSASWV QVSRR
4717	35085	C	4758	150	491	

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4718	35086	A	4759	1	548	GIAFCLNLIKTLKLPNFKSCVIL LGLLLLYDV/FFVFITPFITKNGE SIMVELAAGPFGNNEKNDGNL VEATGQPSAPHEKLPVVIRVPK LIYFSVMSVCLMPVSILGFGDII VPGLLIAYCRRFDVQTGSSYIY YVSSTVAYAIGMILTFVVLVLM KKGQPALLYLVPCTLITASVVA
4719	35087	B	4760	642	1985	
4720	35088	A	4761	39	252	
4721	35089	A	4762	1	783	
4722	35090	C	4763	218	358	
4723	35091	B	4764	372	374	
4724	35092	B	4765	129	1036	
4725	35093	A	4766	1211	1983	SQSCLLLQEDFAPIAGEQEAEQ HQEDLRALLRASLQGQCSRQP GTRLHGSAPWPGEAQNRSRPLP GDSPSLDRYRGI/SDAVGKSRSG DIGSSLRVEAGDKRTQASPERQ PHCGAHDAQDISGGREIFKPRQ LPGSAIWSIKVGHGSGFPGKRR PRGAGLSGRGGRGRSKLKSGIG AVVLPGVSTADISSNKDDEENS VLDMVVLFSSSDKFTLN/QVCG SFGQGAEGRLLACSQCGQCYH PYCVSIKMDACSSSELKY
4726	35094	A	4767	1	603	MANFNDCVLDKEKVCIAAKFIT HAPAGEFNEVFSDIRLLCNNDS LLRERAARAFAHYNMDQFTPV KMEGCEDQTIIACIESHECQPKN FWNGRWRSEWKFTITPPTAQV VGVLKIQVHYYEDGSVQLVSH KDVQDSLTVSNDAQTAKEFIKII ENAENEYQTAISENCQTMSDTT FKVLRRQLPVTRTKIDWNKI\LS YNI
4727	35095	A	4768	1	867	MADFDDRVSDEEKVRIAAKFIT HAPPGEFNEVFNDVRLLLNND NLLREGAAHAFAQYNMDQFH AVK\IEGYEDQVLITEHG\DLGN SRVLDPRNKISF\KFDHLRKEAS DPQPEEADGGLKSWRESCDSA LRAYVKDHYSNGFCTVYAKTI DGQQTIIACIESHQ\FQPKNFWN GR\WRSEWKVP\ITPPSAQ\VVG VLKIQVHYYEDGNVQLVSHKD VQDSLTVSNEAQT\AKEFI\KIIE NAENEYQTAICGNYQTMSDTT FKALRRQLPVTRTKIDWNKILS YKIGKEMQNA

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4728	35096	A	4769	2	690	WPSGSASRPRHLRAPEPV\GKA GKNKGAGLTPA/AGTSGCAGR AESRGPPTGSHGSEPSRGSKGL CGRGTRSLPERGAEVLPHLPAQ TSPQLGSQGAWP/RHPRKPFRP AARAGTQPPGFVPSTPALLKVL YRSAHTQHSGRAAPEPSRLALG PTLQQKRHMGHRRNLTFSSTY NKKCGFGWAVEMRFSALLDVT TTPSRVAFWGSRGPPLGMERQL QLLSGYSPDGWLSTSM
4729	35097	A	4770	1	590	MDTRIGTTDTGTYGKVEGARR MRLKKLPIEYYAYYLDDEIICTS NPCEFPGYGIEREYPCETSGPLE LTVQEDQGEEPQREELTRKKTS KVCRGSPLAWATGVKPCLKKK RRRRKEERRKKKEEGEGEGEEE EEEEEEEEEEEEEEEEEEEEE EE/EEEEEEEEEEEEEEEEEEE EEEEEESDPCTSWNTSQP
4730	35098	A	4771	1	288	
4731	35099	A	4772	1	237	MRSSVIGPRSHIPSQRKSGIQEE EEEEEQEEEEEEEEE/EEEEEEE EEEEEEEEEKGLLDQEAARHLV LPAATQCKPKM
4732	35100	A	4773	1	794	MASHSSPMGSQYYYGFPGPDS AMHALNTVVSEKDLTLDLSGL VARNKRCGPHSYSLNTHLLHA CLRLPTQRENTTLKTFIPQGWEI HTDQVEREAECQPGRLKICVHD TAQELPLASTARNALLGRNLCP FRQSSTTQMPDEIPISLDDRMRP PSLKKKK/VVGEEEEEEE\EKEK EEEEEE/DEGEEEEEEEEEEEE EEEEEEEEEEGGGGGVGEEEEE EEGEGEGGGGEEDEEE*EEEEE EQKKKEKKKKEQEEGGGEGG
4733	35101	A	4774	115	341	
4734	35102	A	4775	1	651	
4735	35103	A	4776	189	618	SLCHKEAEGGHGKAHVEGKRA PSNLQPSAPAELSGNNSISF\HHE EEEEEEEEEEEEEEEEEEEEE EEEEEEEEEEEEEEEEDLLYNFI YIIFSKMPTKVPSLWDSKLGAE QAAPEENNKKEQQEEYQGKSF SFLNLTECWP
4736	35104	A	4777	1	414	

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4737	35105	A	4778	189	692	SLCHKEAEGGHGKAHVEGKRA PSNLQPSAPAELSGNNSISF\HHE EEEEEEEEEEEEEEEEEEEEE EEEEEEEEEEEEEEEEDLLYNF IYIIFSKMPTKAMSISSMFKFAT KIRMTVTPNPKCCWIPVFPAYL STSKAAKCMHHTAHHGQEKSD HCISPSPIPAP
4738	35106	A	4779	2	3815	
4739	35107	A	4780	957	1493	KNRNYNKLSLRPQCNPTRTQD* ETHSKPLNYMETEQPSPE*LLG T*RNEGRHKAVL*NQ*EKRHNI PESLGHI/AKQCVEGNL*H*MPT RESRKDLKLTP*/PSQLKELEKQ EQTHSKAGRRQE/TN*DQSRIEG DRDTKNPSKNQ*IQELVF*KDQ QN**TASKTNKEEKREESNRRN KKC
4740	35108	A	4781	1	4962	
4741	35109	A	4782	2421	3011	NQACQPGQAGAARAGQCFPRV AQRPGPGPAGMALAHPDLYLC HSAGDQCR*DEEADPPEGQAPT HFQVHPAGGLHLLDRLAAPQH QAGTQGQGQPGRHH*PAARSS PVEPPSTGSPSRPTTTMWPSCSR RQGGLGPGL*CVQQPHLLDAP GTLPVLGALVCRLQPWRCLPL GGGGGVGGSQRPPGGGGGNG GRNWG
4742	35110	A	4783	1	932	MRTPKSSIKPSLGEEKENYRGS LKETAPSLQKEWAEQSSKSQET VGVKGITRHFQVSTLLERREDR KSKEPPLLIPRQTVSGVDLQQTP TDLQLSVLTVRRKTNKQKGHP HQKPICTSPSSNTKVKNLEKQL DEWLTRITNAEKSSKDRMELKT KARELHDECTSLSSRCDQLEER VSVTEDEMNEMKRGEKFREKR IKRNEQSLQEIWDYVKRPNLCL IGVPESDGENGTKLENTLQDIIQ ENFPNLARQANIQIQEI/RENAT KILLEKSNSKTHNCQIHQS*NEG KNVKGSQRERSGYPQREAHQT
4743	35111	A	4784	477	638	LLCCGFELPLLARRSLIV*SLLLS THQSHSPSSFVPLLVRSCIPLEEE RRSDF
4744	35112	B	4785	1	1509	

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4745	35113	A	4786	3	832	ERHHPPPQAGPHPPRRRKERNT HRQPTPQPHGA/WKISVPQTTN KGISSSITSTQRNQPQATTVEKA HNESTRTPEEPKGAVRGTR*KK KKTSRDTPPQTP*EKSSSATRNK AGGKDSDKRERKATEDQTTPS KRRKLHPMAKKLKTLKKN*MN G*LE*PMQRSP*RT*WS*KPRHE NYVMNAQASVTDAINWKKGPP PRPTTNDAKIVTRPTHPTCSHH RPPRKPPRTHPTPTPTQNKISQ* NGYTPPRGKRVREDRCKPPQAP TSAPRAAKQRQS
4746	35114	B	4787	1580	4673	
4747	35115	A	4788	1	462	MKLEHQEAQRRSGQGREKRR WPEGKAGPGCEGAWILCPESQ DDSKQEGDNNMIVVSRNAVRS VKAEFQGDNLENWESCSEAIIV QGRDNGVPHKAHGLGTEEEGT VLKISERQNWLDLVDFILLGGD LFHENKPSRKTLHTCLELLRKY CMGDRPVQFEILSDQSVNFGFR KLTNRKDIHTKNPSVRHHHQRP KVDETIKMGKTQSRKTRNSKN QSTSPPPKERSSSPAIEQSWMEN DFDELKEEGFRRSNYSELKEEV RTNGKEVKNLEKKLDKWITRIT NAEKSLKDLMELKTIAQELRDE CTSLSNQCDQLEERVSVMEDQ MNEMKREEKFREKRIKRNEQS LQEIWDYVKRPNLCLIGVPESD GENGTKLENTLQDIIQVNFPNL ARQANIQIQEIQRMPQRYSLRR ETPRHIIVRFTKVEMKEKMLRT AREKGLECSGAGLAHCKLWLL GPSDPPDCSSVSPVLRVHLVLPS SLPHSVGTPFLGSVSIPPSVPRFP DRVFHPYPYTHYCDNLKTCHT SHGSVMAETAVINHKKRKNSP RIVQSNDLTEAAYSLSRDQKRM LYLFVDQIRKSDGTLQEHDGIC EIHVAKYAEIFGLTSAEASKDIR QALKSFAGKEVVFYRPEEDAG DEKGYESFPWFIKRAHSPSRGL YSVHINPYLIPFFIGLQNRFTQFR LSETKEITNPYAMRLYESLCQY

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4748	35116	A	4789	1314	2221	KNRNYNKLSLRPQCNPTRTQD* ETHSKPLNYMETEQPSPE*LLG T*RNEGRHKAVL*NQ*EKRHNI PESLGHI/AKQCVEGNL*H*MPT RESRKDLKLTP*/PSQLKELEKQ EQTHSKAGRRQE/TN*DQSRIEG DRDTKNPSKNQ*IQELVF*KDQ QN**TASKT/IQRRKERRIK*TQ* KMLKEDITTDPTEIKTIIREYYK HLYAHNLENLEEMDKFLDTYT LPRLNQEEAESLNRPITNSEIET VINSLKEKAQDQKDLQLNSTRA LFTIAKAWNQPKCPSMTDEIK/I NVEHIHHGILCSHQKE
4749	35117	A	4790	2	2260	TKDKNHMIISIDGGKAFDKIQQ PFMLKTLNKLGIDGTYLKRIRAI FDKPTANIILNGQKLEAFPLKTG TRQGCPLSPLLFNIVLEVLARVI RQEKEIKGIQFGKEEVKLSLFA DDMTVYLENPIFSAQNLLKLIS NFSNVSGYKINVQKSQAFLYTN NSQIMSELPFTIATKRITYLGIQL ARDVKDLFKENYKPLLNEIKED TNKWKNIPCSQIGRILWPYCPR QEDENFNSLLQNGDILNSSTEE KFKAHDKKDFNLPEYDLNVEE RLVLIEKSVDSTATADDTHKLD HINMNLNKLITNDTFQPEIMERS KTQDIVLGTSFLSINSKEETEHL ENGNKYPNLESVNKVNGHSEE TSQSPNRTEPHDSDCSVDLGISK STEDLSPQKSGPVGSVVKSHSIT NMEIGGLKIYDILSDNGPQQPST TVKITSAVDGKNIVRSKSATLL YDQPLQVFTGSSSSSDLISGTKA IFKFDSNHNPEEPNIIRGPTSGPQ SAPQI\YGPPQYNIQYSSSAAVK DTLWHSKQNPQIDHASFPPQLL PRSESTENQSYAKHSANMNFSN HNNVRANTAYHLHQRLGPARH GEMWAISPNDRLIPAVTRSTIQR QSSVSSTASVNLGDPGSTRRAQ IPEGDYLSYREFHSAGRTPPMM PGSQRPLSARTYSIDGPNASRPQ SARPSINEIPERTMSVSDFNYSR TSPSKRPNARVGSEHSLLDPPG
4750	35118	A	4791	1516	1729	ILAPHSLLACRVSAERSAVSPM GFPLWVTQPFSLAALN/DFFLHF NFG/RI*QLCVLELLFSRSIVVAF SEFP